Sequence Listing

<110> Avi J. Ashkenazi
Kevin P. Baker
David Botstein
Luc Desnoyers
Dan L. Eaton
Napoleone Ferrara
Sherman Fong
Wei-Qiang Gao
Hanspeter Gerber
Mary E. Gerritsen
Audrey Goddard
Paul J. Godowski
Austin L. Gurney
Ivar J. Kljavin
Jennie P. Mather
Mary A. Napier
James Pan
Nicholas F. Paoni
Margaret Ann Roy
Timothy A. Stewart
Daniel Tumas
Colin K. Watanabe
P.Mickey Williams
William I. Wood
Zemin Zang

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Ala Arg Glu Gln His Trp Asp Arg Pro Ser Ala Ser Arg Arg Arg
20 25 30

Ser Ser Pro Ser Lys Asn Arg Gly Leu Cys Asn Gly Asn Leu Val
35 40 45

Asp Ile Phe Ser Lys Val Arg Ile Phe Gly Leu Lys Lys Arg Arg
50 55 60

Leu Arg Arg Gln Asp Pro Gln Leu Lys Gly Ile Val Thr Arg Leu
65 70 75

Tyr Cys Arg Gln Gly Tyr Tyr Leu Gln Met His Pro Asp Gly Ala
80 85 90

Leu Asp Gly Thr Lys Asp Asp Ser Thr Asn Ser Thr Leu Phe Asn
95 100 105

Leu Ile Pro Val Gly Leu Arg Val Val Ala Ile Gln Gly Val Lys
110 115 120

Thr Gly Leu Tyr Ile Ala Met Asn Gly Glu Gly Tyr Leu Tyr Pro
125 130 135

Ser Glu Leu Phe Thr Pro Glu Cys Lys Phe Lys Glu Ser Val Phe
140 145 150

Glu Asn Tyr Tyr Val Ile Tyr Ser Ser Met Leu Tyr Arg Gln Gln
155 160 165

Glu Ser Gly Arg Ala Trp Phe Leu Gly Leu Asn Lys Glu Gly Gln
170 175 180

Ala Met Lys Gly Asn Arg Val Lys Lys Thr Lys Pro Ala Ala His
185 190 195

Phe Leu Pro Lys Pro Leu Glu Val Ala Met Tyr Arg Glu Pro Ser
200 205 210

Leu His Asp Val Gly Glu Thr Val Pro Lys Pro Gly Val Thr Pro
215 220 225

Ser Lys Ser Thr Ser Ala Ser Ala Ile Met Asn Gly Gly Lys Pro
230 235 240

Val Asn Lys Ser Lys Thr Thr
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<210> 14
<211> 2609
<212> DNA
<213> Homo Sapien

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tgagcgctgt aatctgaacc agctgtgtcc agactgaggc cccatttgca 150

ttgtttaaca tacttagaaa atgaagtgtt catttttaac attcctcctc 200

caattggttt aatgctgaat tactgaagag ggctaagcaa aaccaggtgc 250

ttgcgctgag ggctctgcag tggctgggag gaccccggcg ctctccccgt 300

gtcctctcca cgactcgctc ggcccctctg gaataaaaca cccgcgagcc 350

ccgagggccc agaggaggcc gacgtgcccg agctcctccg gggtcccgc 400

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<210> 15
<211> 448
<212> PRT
<213> Homo Sapien

<400> 15

Met	Pro	Gly	Ile	Lys	Arg	Ile	Leu	Thr	Val	Thr	Ile	Leu	Ala	Leu	
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Cys	Leu	Pro	Ser	Pro	Gly	Asn	Ala	Gln	Ala	Gln	Cys	Thr	Asn	Gly	
				20				25						30	
Phe	Asp	Leu	Asp	Arg	Gln	Ser	Gly	Gln	Cys	Leu	Asp	Ile	Asp	Glu	
				35				40						45	
Cys	Arg	Thr	Ile	Pro	Glu	Ala	Cys	Arg	Gly	Asp	Met	Met	Cys	Val	
				50				55						60	

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Asn Gln Asn Gly Gly Tyr Leu Cys Ile Pro Arg Thr Asn Pro Val
                65                  70                  75

Tyr Arg Gly Pro Tyr Ser Asn Pro Tyr Ser Thr Pro Tyr Ser Gly
                80                  85                  90

Pro Tyr Pro Ala Ala Ala Pro Pro Leu Ser Ala Pro Asn Tyr Pro
                95                 100                 105

Thr Ile Ser Arg Pro Leu Ile Cys Arg Phe Gly Tyr Gln Met Asp
               110                 115                 120

Glu Ser Asn Gln Cys Val Asp Val Asp Glu Cys Ala Thr Asp Ser
               125                 130                 135

His Gln Cys Asn Pro Thr Gln Ile Cys Ile Asn Thr Glu Gly Gly
               140                 145                 150

Tyr Thr Cys Ser Cys Thr Asp Gly Tyr Trp Leu Leu Glu Gly Gln
               155                 160                 165

Cys Leu Asp Ile Asp Glu Cys Arg Tyr Gly Tyr Cys Gln Gln Leu
               170                 175                 180

Cys Ala Asn Val Pro Gly Ser Tyr Ser Cys Thr Cys Asn Pro Gly
               185                 190                 195

Phe Thr Leu Asn Glu Asp Gly Arg Ser Cys Gln Asp Val Asn Glu
               200                 205                 210

Cys Ala Thr Glu Asn Pro Cys Val Gln Thr Cys Val Asn Thr Tyr
               215                 220                 225

Gly Ser Leu Ile Cys Arg Cys Asp Pro Gly Tyr Glu Leu Glu Glu
               230                 235                 240

Asp Gly Val His Cys Ser Asp Met Asp Glu Cys Ser Phe Ser Glu
               245                 250                 255

Phe Leu Cys Gln His Glu Cys Val Asn Gln Pro Gly Thr Tyr Phe
               260                 265                 270

Cys Ser Cys Pro Pro Gly Tyr Ile Leu Leu Asp Asp Asn Arg Ser
               275                 280                 285

Cys Gln Asp Ile Asn Glu Cys Glu His Arg Asn His Thr Cys Asn
               290                 295                 300

Leu Gln Gln Thr Cys Tyr Asn Leu Gln Gly Gly Phe Lys Cys Ile
               305                 310                 315

Asp Pro Ile Arg Cys Glu Glu Pro Tyr Leu Arg Ile Ser Asp Asn
               320                 325                 330

Arg Cys Met Cys Pro Ala Glu Asn Pro Gly Cys Arg Asp Gln Pro
               335                 340                 345

Phe Thr Ile Leu Tyr Arg Asp Met Asp Val Val Ser Gly Arg Ser
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350 355 360

Val Pro Ala Asp Ile Phe Gln Met Gln Ala Thr Thr Arg Tyr Pro
365 370 375

Gly Ala Tyr Tyr Ile Phe Gln Ile Lys Ser Gly Asn Glu Gly Arg
380 385 390

Glu Phe Tyr Met Arg Gln Thr Gly Pro Ile Ser Ala Thr Leu Val
395 400 405

Met Thr Arg Pro Ile Lys Gly Pro Arg Glu Ile Gln Leu Asp Leu
410 415 420

Glu Met Ile Thr Val Asn Thr Val Ile Asn Phe Arg Gly Ser Ser
425 430 435

Val Ile Arg Leu Arg Ile Tyr Val Ser Gln Tyr Pro Phe
440 445

<210> 16
<211> 2447
<212> DNA
<213> Homo Sapien

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gggctcctcc ctgccgcctc ctctcagtgg atggttccag gcaccctgtc 200

tggggcaggg agggcacagg cctgcacatc gaaggtgggg tgggaccagg 250

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ccaaaaaaaa aaaaaaaaaa gggcggccgc gactctagag tcgacct 2447

<210> 17
<211> 428
<212> PRT
<213> Homo Sapien

<400> 17

Met	Gln	Glu	Leu	His	Leu	Leu	Trp	Trp	Ala	Leu	Leu	Leu	Gly	Leu	
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Ala	Gln	Ala	Cys	Pro	Glu	Pro	Cys	Asp	Cys	Gly	Glu	Lys	Tyr	Gly	
				20					25						30
Phe	Gln	Ile	Ala	Asp	Cys	Ala	Tyr	Arg	Asp	Leu	Glu	Ser	Val	Pro	
				35					40						45
Pro	Gly	Phe	Pro	Ala	Asn	Val	Thr	Thr	Leu	Ser	Leu	Ser	Ala	Asn	
				50					55						60
Arg	Leu	Pro	Gly	Leu	Pro	Glu	Gly	Ala	Phe	Arg	Glu	Val	Pro	Leu	
				65					70						75
Leu	Gln	Ser	Leu	Trp	Leu	Ala	His	Asn	Glu	Ile	Arg	Thr	Val	Ala	
				80					85						90
Ala	Gly	Ala	Leu	Ala	Ser	Leu	Ser	His	Leu	Lys	Ser	Leu	Asp	Leu	
				95					100						105
Ser	His	Asn	Leu	Ile	Ser	Asp	Phe	Ala	Trp	Ser	Asp	Leu	His	Asn	
				110					115						120
Leu	Ser	Ala	Leu	Gln	Leu	Leu	Lys	Met	Asp	Ser	Asn	Glu	Leu	Thr	
				125					130						135
Phe	Ile	Pro	Arg	Asp	Ala	Phe	Arg	Ser	Leu	Arg	Ala	Leu	Arg	Ser	
				140					145						150
Leu	Gln	Leu	Asn	His	Asn	Arg	Leu	His	Thr	Leu	Ala	Glu	Gly	Thr	
				155					160						165
Phe	Thr	Pro	Leu	Thr	Ala	Leu	Ser	His	Leu	Gln	Ile	Asn	Glu	Asn	
				170					175						180
Pro	Phe	Asp	Cys	Thr	Cys	Gly	Ile	Val	Trp	Leu	Lys	Thr	Trp	Ala	
				185					190						195
Leu	Thr	Thr	Ala	Val	Ser	Ile	Pro	Glu	Gln	Asp	Asn	Ile	Ala	Cys	
				200					205						210
Thr	Ser	Pro	His	Val	Leu	Lys	Gly	Thr	Pro	Leu	Ser	Arg	Leu	Pro	
				215					220						225

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Pro Leu Pro Cys Ser Ala Pro Ser Val Gln Leu Ser Tyr Gln Pro
                230                 235                 240

Ser Gln Asp Gly Ala Glu Leu Arg Pro Gly Phe Val Leu Ala Leu
                245                 250                 255

His Cys Asp Val Asp Gly Gln Pro Ala Pro Gln Leu His Trp His
                260                 265                 270

Ile Gln Ile Pro Ser Gly Ile Val Glu Ile Thr Ser Pro Asn Val
                275                 280                 285

Gly Thr Asp Gly Arg Ala Leu Pro Gly Thr Pro Val Ala Ser Ser
                290                 295                 300

Gln Pro Arg Phe Gln Ala Phe Ala Asn Gly Ser Leu Leu Ile Pro
                305                 310                 315

Asp Phe Gly Lys Leu Glu Glu Gly Thr Tyr Ser Cys Leu Ala Thr
                320                 325                 330

Asn Glu Leu Gly Ser Ala Glu Ser Ser Val Asp Val Ala Leu Ala
                335                 340                 345

Thr Pro Gly Glu Gly Gly Glu Asp Thr Leu Gly Arg Arg Phe His
                350                 355                 360

Gly Lys Ala Val Glu Gly Lys Gly Cys Tyr Thr Val Asp Asn Glu
                365                 370                 375

Val Gln Pro Ser Gly Pro Glu Asp Asn Val Val Ile Ile Tyr Leu
                380                 385                 390

Ser Arg Ala Gly Asn Pro Glu Ala Ala Val Ala Glu Gly Val Pro
                395                 400                 405

Gly Gln Leu Pro Pro Gly Leu Leu Leu Leu Gly Gln Ser Leu Leu
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Leu Phe Phe Phe Leu Thr Ser Phe
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<210> 18
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 18
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<210> 19
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<212> DNA
<213> Artificial Sequence
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<223> Synthetic oligonucleotide probe

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<210> 20
<211> 50
<212> DNA
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<223> Synthetic oligonucleotide probe

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<210> 21
<211> 2033
<212> DNA
<213> Homo Sapien

<400> 21
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agaagatatc ctgattgttt cagaggggaa aatggcacct tttacacatg 350

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<210> 22
<211> 379
<212> PRT
<213> Homo Sapien

<400> 22
Met Ala Arg Arg Ser Ala Phe Pro Ala Ala Ala Leu Trp Leu Trp
1 5 10 15

Ser Ile Leu Leu Cys Leu Leu Ala Leu Arg Ala Glu Ala Gly Pro
20 25 30

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Pro Gln Glu Glu Ser Leu Tyr Leu Trp Ile Asp Ala His Gln Ala
                35                  40                  45

Arg Val Leu Ile Gly Phe Glu Glu Asp Ile Leu Ile Val Ser Glu
                50                  55                  60

Gly Lys Met Ala Pro Phe Thr His Asp Phe Arg Lys Ala Gln Gln
                65                  70                  75

Arg Met Pro Ala Ile Pro Val Asn Ile His Ser Met Asn Phe Thr
                80                  85                  90

Trp Gln Ala Ala Gly Gln Ala Glu Tyr Phe Tyr Glu Phe Leu Ser
                95                 100                 105

Leu Arg Ser Leu Asp Lys Gly Ile Met Ala Asp Pro Thr Val Asn
               110                 115                 120

Val Pro Leu Leu Gly Thr Val Pro His Lys Ala Ser Val Val Gln
               125                 130                 135

Val Gly Phe Pro Cys Leu Gly Lys Gln Asp Gly Val Ala Ala Phe
               140                 145                 150

Glu Val Asp Val Ile Val Met Asn Ser Glu Gly Asn Thr Ile Leu
               155                 160                 165

Gln Thr Pro Gln Asn Ala Ile Phe Phe Lys Thr Cys Gln Gln Ala
               170                 175                 180

Glu Cys Pro Gly Gly Cys Arg Asn Gly Gly Phe Cys Asn Glu Arg
               185                 190                 195

Arg Ile Cys Glu Cys Pro Asp Gly Phe His Gly Pro His Cys Glu
               200                 205                 210

Lys Ala Leu Cys Thr Pro Arg Cys Met Asn Gly Gly Leu Cys Val
               215                 220                 225

Thr Pro Gly Phe Cys Ile Cys Pro Pro Gly Phe Tyr Gly Val Asn
               230                 235                 240

Cys Asp Lys Ala Asn Cys Ser Thr Thr Cys Phe Asn Gly Gly Thr
               245                 250                 255

Cys Phe Tyr Pro Gly Lys Cys Ile Cys Pro Pro Gly Leu Glu Gly
               260                 265                 270

Glu Gln Cys Glu Ile Ser Lys Cys Pro Gln Pro Cys Arg Asn Gly
               275                 280                 285

Gly Lys Cys Ile Gly Lys Ser Lys Cys Lys Cys Ser Lys Gly Tyr
               290                 295                 300

Gln Gly Asp Leu Cys Ser Lys Pro Val Cys Glu Pro Gly Cys Gly
               305                 310                 315

Ala His Gly Thr Cys His Glu Pro Asn Lys Cys Gln Cys Gln Glu
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320 325 330

Gly Trp His Gly Arg His Cys Asn Lys Arg Tyr Glu Ala Ser Leu
335 340 345

Ile His Ala Leu Arg Pro Ala Gly Ala Gln Leu Arg Gln His Thr
350 355 360

Pro Ser Leu Lys Lys Ala Glu Glu Arg Arg Asp Pro Pro Glu Ser
365 370 375

Asn Tyr Ile Trp

<210> 23
<211> 783
<212> DNA
<213> Homo Sapien

<400> 23
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ctggaattga ggctgagcca aagaccccag ggccgtctca gtctcataaa 200

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gaagctatga attcaccagt aacagctgct cccagcgggc tgtgatattc 450

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tgaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 750

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 783

<210> 24
<211> 94
<212> PRT
<213> Homo Sapien

<400> 24

Met Met Gly Leu Ser Leu Ala Ser Ala Val Leu Leu Ala Ser Leu
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Leu Ser Leu His Leu Gly Thr Ala Thr Arg Gly Ser Asp Ile Ser
20 25 30

Lys Thr Cys Cys Phe Gln Tyr Ser His Lys Pro Leu Pro Trp Thr
35 40 45

Trp Val Arg Ser Tyr Glu Phe Thr Ser Asn Ser Cys Ser Gln Arg
50 55 60

Ala Val Ile Phe Thr Thr Lys Arg Gly Lys Lys Val Cys Thr His
65 70 75

Pro Arg Lys Lys Trp Val Gln Lys Tyr Ile Ser Leu Leu Lys Thr
80 85 90

Pro Lys Gln Leu

<210> 25
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 25
ggatcaggca ggaggagttt ggg 23

<210> 26
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 26
ggatgggtac agactttctt gcc 23

<210> 27
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 27
atgatgggcc tctccttggc ctctgctgtg ctcctggcct ccctcctgag 50

<210> 28
<211> 3552
<212> DNA
<213> Homo Sapien

<400> 28
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ggacagcgtc gggaaccaga ccatggctcc tggaccccaa gatccttaag 200

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caccatcccc cggcaggacg aagttcccca gcagacagtg gccccacagc 300

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tcagaatata ctggagcctg taacccgtgc acagagggtg tggattacac 400

cattgcttcc aacaatttgc cttcttgcct gctatgtaca gtttgtaaat 450

caggtcaaac aaataaaagt tcctgtacca cgaccagaga caccgtgtgt 500

cagtgtgaaa aaggaagctt ccaggataaa aactcccctg agatgtgccg 550

gacgtgtaga acagggtgtc ccagagggat ggtcaaggtc agtaattgta 600

cgccccggag tgacatcaag tgcaaaaatg aatcagctgc cagttccact 650

gggaaaaccc cagcagcgga ggagacagtg accaccatcc tggggatgct 700

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<210> 29
<211> 386
<212> PRT
<213> Homo Sapien

<400> 29

Met Gly Leu Trp Gly Gln Ser Val Pro Thr Ala Ser Ser Ala Arg
1 5 10 15

Ala Gly Arg Tyr Pro Gly Ala Arg Thr Ala Ser Gly Thr Arg Pro
20 25 30

Trp Leu Leu Asp Pro Lys Ile Leu Lys Phe Val Val Phe Ile Val
35 40 45

Ala Val Leu Leu Pro Val Arg Val Asp Ser Ala Thr Ile Pro Arg
50 55 60

Gln Asp Glu Val Pro Gln Gln Thr Val Ala Pro Gln Gln Gln Arg
65 70 75

Arg Ser Leu Lys Glu Glu Glu Cys Pro Ala Gly Ser His Arg Ser
80 85 90

Glu Tyr Thr Gly Ala Cys Asn Pro Cys Thr Glu Gly Val Asp Tyr
95 100 105

Thr Ile Ala Ser Asn Asn Leu Pro Ser Cys Leu Leu Cys Thr Val
110 115 120

Cys Lys Ser Gly Gln Thr Asn Lys Ser Ser Cys Thr Thr Thr Arg
125 130 135

Asp Thr Val Cys Gln Cys Glu Lys Gly Ser Phe Gln Asp Lys Asn
140 145 150

Ser Pro Glu Met Cys Arg Thr Cys Arg Thr Gly Cys Pro Arg Gly
155 160 165

Met Val Lys Val Ser Asn Cys Thr Pro Arg Ser Asp Ile Lys Cys
170 175 180

Lys Asn Glu Ser Ala Ala Ser Ser Thr Gly Lys Thr Pro Ala Ala
185 190 195

Glu Glu Thr Val Thr Thr Ile Leu Gly Met Leu Ala Ser Pro Tyr
200 205 210

His Tyr Leu Ile Ile Ile Val Val Leu Val Ile Ile Leu Ala Val
215 220 225

Val Val Val Gly Phe Ser Cys Arg Lys Lys Phe Ile Ser Tyr Leu
230 235 240

Lys Gly Ile Cys Ser Gly Gly Gly Gly Gly Pro Glu Arg Val His
245 250 255

Arg Val Leu Phe Arg Arg Arg Ser Cys Pro Ser Arg Val Pro Gly
260 265 270

Ala Glu Asp Asn Ala Arg Asn Glu Thr Leu Ser Asn Arg Tyr Leu
275 280 285

Gln Pro Thr Gln Val Ser Glu Gln Glu Ile Gln Gly Gln Glu Leu
290 295 300

Ala Glu Leu Thr Gly Val Thr Val Glu Ser Pro Glu Glu Pro Gln
305 310 315

Arg Leu Leu Glu Gln Ala Glu Ala Glu Gly Cys Gln Arg Arg Arg
320 325 330

Leu Leu Val Pro Val Asn Asp Ala Asp Ser Ala Asp Ile Ser Thr
335 340 345

Leu Leu Asp Ala Ser Ala Thr Leu Glu Glu Gly His Ala Lys Glu
350 355 360

Thr Ile Gln Asp Gln Leu Val Gly Ser Glu Lys Leu Phe Tyr Glu
365 370 375

Glu Asp Glu Ala Gly Ser Ala Thr Ser Cys Leu
380 385

<210> 30
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 30
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<210> 31
<211> 963
<212> DNA
<213> Homo Sapien

<400> 31
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ttcgtggtct tcgcctcctt gtgtgcctgg tattcggggt acctgctcgc 100

agagctcatt ccagatgcac ccctgtccag tgctgcctat agcatccgca 150

gcatcgggga gaggcctgtc ctcaaagctc cagtccccaa aaggcaaaaa 200

tgtgaccact ggactccctg cccatctgac acctatgcct acaggttact 250

cagcggaggt ggcagaagca agtacgccaa aatctgcttt gaggataacc 300

tacttatggg agaacagctg ggaaatgttg ccagaggaat aaacattgcc 350

attgtcaact atgtaactgg gaatgtgaca gcaacacgat gttttgatat 400

gtatgaaggc gataactctg gaccgatgac aaagtttatt cagagtgctg 450

ctccaaaatc cctgctcttc atggtgacct atgacgacgg aagcacaaga 500

ctgaataacg atgccaagaa tgccatagaa gcacttggaa gtaaagaaat 550

caggaacatg aaattcaggt ctagctgggt atttattgca gcaaaaggct 600

tggaactccc ttccgaaatt cagagagaaa agatcaacca ctctgatgct 650

aagaacaaca gatattctgg ctggcctgca gagatccaga tagaaggctg 700

catacccaaa gaacgaagct gacactgcag ggtcctgagt aaatgtgttc 750

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cttaaaaaaa aaa 963

<210> 32
<211> 235
<212> PRT
<213> Homo Sapien

<400> 32

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Met Arg Pro Leu Ala Gly Gly Leu Leu Lys Val Val Phe Val Val
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Phe Ala Ser Leu Cys Ala Trp Tyr Ser Gly Tyr Leu Leu Ala Glu
             20                  25                  30

Leu Ile Pro Asp Ala Pro Leu Ser Ser Ala Ala Tyr Ser Ile Arg
             35                  40                  45

Ser Ile Gly Glu Arg Pro Val Leu Lys Ala Pro Val Pro Lys Arg
             50                  55                  60

Gln Lys Cys Asp His Trp Thr Pro Cys Pro Ser Asp Thr Tyr Ala
             65                  70                  75

Tyr Arg Leu Leu Ser Gly Gly Gly Arg Ser Lys Tyr Ala Lys Ile
             80                  85                  90

Cys Phe Glu Asp Asn Leu Leu Met Gly Glu Gln Leu Gly Asn Val
             95                 100                 105

Ala Arg Gly Ile Asn Ile Ala Ile Val Asn Tyr Val Thr Gly Asn
            110                 115                 120

Val Thr Ala Thr Arg Cys Phe Asp Met Tyr Glu Gly Asp Asn Ser
            125                 130                 135

Gly Pro Met Thr Lys Phe Ile Gln Ser Ala Ala Pro Lys Ser Leu
            140                 145                 150

Leu Phe Met Val Thr Tyr Asp Asp Gly Ser Thr Arg Leu Asn Asn
            155                 160                 165

Asp Ala Lys Asn Ala Ile Glu Ala Leu Gly Ser Lys Glu Ile Arg
            170                 175                 180

Asn Met Lys Phe Arg Ser Ser Trp Val Phe Ile Ala Ala Lys Gly
            185                 190                 195

Leu Glu Leu Pro Ser Glu Ile Gln Arg Glu Lys Ile Asn His Ser
            200                 205                 210

Asp Ala Lys Asn Asn Arg Tyr Ser Gly Trp Pro Ala Glu Ile Gln
            215                 220                 225

Ile Glu Gly Cys Ile Pro Lys Glu Arg Ser
            230                 235
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<210> 33
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 33
ggctggcctg cagagatc 18

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<210> 34
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 34
aatgtgacca ctggactccc 20

<210> 35
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 35
aggcttggaa ctcccttc 18

<210> 36
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 36
aagattcttg agcgattcca gctg 24

<210> 37
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 37
aatccctgct cttcatggtg acctatgacg acggaagcac aagactg 47

<210> 38
<211> 1215
<212> DNA
<213> Homo Sapien

<400> 38
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gagccccaca ggacggcatc agaattaatg taactacact gaaagatgat 300

ggggacatat ctaaacagca ggttgttctt aacataacct atgagagtgg 350

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gctgtcagac tttgatagtg aagaatgaaa atcttgaaaa tttggaggaa 450

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<210> 39
<211> 330
<212> PRT
<213> Homo Sapien

<400> 39
Met Glu Gly Ala Pro Pro Gly Ser Leu Ala Leu Arg Leu Leu Leu
1 5 10 15

Phe Val Ala Leu Pro Ala Ser Gly Trp Leu Thr Thr Gly Ala Pro
20 25 30

Glu Pro Pro Pro Leu Ser Gly Ala Pro Gln Asp Gly Ile Arg Ile
35 40 45

Asn Val Thr Thr Leu Lys Asp Asp Gly Asp Ile Ser Lys Gln Gln

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                50                  55                  60

Val Val Leu Asn Ile Thr Tyr Glu Ser Gly Gln Val Tyr Val Asn
                65                  70                  75

Asp Leu Pro Val Asn Ser Gly Val Thr Arg Ile Ser Cys Gln Thr
                80                  85                  90

Leu Ile Val Lys Asn Glu Asn Leu Glu Asn Leu Glu Glu Lys Glu
                95                 100                 105

Tyr Phe Gly Ile Val Ser Val Arg Ile Leu Val His Glu Trp Pro
               110                 115                 120

Met Thr Ser Gly Ser Ser Leu Gln Leu Ile Val Ile Gln Glu Glu
               125                 130                 135

Val Val Glu Ile Asp Gly Lys Gln Val Gln Gln Lys Asp Val Thr
               140                 145                 150

Glu Ile Asp Ile Leu Val Lys Asn Arg Gly Val Leu Arg His Ser
               155                 160                 165

Asn Tyr Thr Leu Pro Leu Glu Glu Ser Met Leu Tyr Ser Ile Ser
               170                 175                 180

Arg Asp Ser Asp Ile Leu Phe Thr Leu Pro Asn Leu Ser Lys Lys
               185                 190                 195

Glu Ser Val Ser Ser Leu Gln Thr Thr Ser Gln Tyr Leu Ile Arg
               200                 205                 210

Asn Val Glu Thr Thr Val Asp Glu Asp Val Leu Pro Gly Lys Leu
               215                 220                 225

Pro Glu Thr Pro Leu Arg Ala Glu Pro Pro Ser Ser Tyr Lys Val
               230                 235                 240

Met Cys Gln Trp Met Glu Lys Phe Arg Lys Asp Leu Cys Arg Phe
               245                 250                 255

Trp Ser Asn Val Phe Pro Val Phe Phe Gln Phe Leu Asn Ile Met
               260                 265                 270

Val Val Gly Ile Thr Gly Ala Ala Val Val Ile Thr Ile Leu Lys
               275                 280                 285

Val Phe Phe Pro Val Ser Glu Tyr Lys Gly Ile Leu Gln Leu Asp
               290                 295                 300

Lys Val Asp Val Ile Pro Val Thr Ala Ile Asn Leu Tyr Pro Asp
               305                 310                 315

Gly Pro Glu Lys Arg Ala Glu Asn Leu Glu Asp Lys Thr Cys Ile
               320                 325                 330
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<210> 40
<211> 2498

<212> DNA
<213> Homo Sapien

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ggccacctgc agcctggtgc tccagactga tgtcacccgg gccgagtgct 200

gtgcctccgg caacattgac accgcctggt ccaacctcac ccacccgggg 250

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tggggccctg cctcaccaag gaaataaaga ctcaagccat aaaaaaaa 2498

<210> 41
<211> 263
<212> PRT
<213> Homo Sapien

<400> 41

Met	Arg	Pro	Gly	Ala	Pro	Gly	Pro	Leu	Trp	Pro	Leu	Pro	Trp	Gly
1				5				10						15

Ala	Leu	Ala	Trp	Ala	Val	Gly	Phe	Val	Ser	Ser	Met	Gly	Ser	Gly
			20					25						30

Asn Pro Ala Pro Gly Gly Val Cys Trp Leu Gln Gln Gly Gln Glu
35 40 45

Ala Thr Cys Ser Leu Val Leu Gln Thr Asp Val Thr Arg Ala Glu
50 55 60

Cys Cys Ala Ser Gly Asn Ile Asp Thr Ala Trp Ser Asn Leu Thr
65 70 75

His Pro Gly Asn Lys Ile Asn Leu Leu Gly Phe Leu Gly Leu Val
80 85 90

His Cys Leu Pro Cys Lys Asp Ser Cys Asp Gly Val Glu Cys Gly
95 100 105

Pro Gly Lys Ala Cys Arg Met Leu Gly Gly Arg Pro Arg Cys Glu
110 115 120

Cys Ala Pro Asp Cys Ser Gly Leu Pro Ala Arg Leu Gln Val Cys
125 130 135

Gly Ser Asp Gly Ala Thr Tyr Arg Asp Glu Cys Glu Leu Arg Ala
140 145 150

Ala Arg Cys Arg Gly His Pro Asp Leu Ser Val Met Tyr Arg Gly
155 160 165

Arg Cys Arg Lys Ser Cys Glu His Val Val Cys Pro Arg Pro Gln
170 175 180

Ser Cys Val Val Asp Gln Thr Gly Ser Ala His Cys Val Val Cys
185 190 195

Arg Ala Ala Pro Cys Pro Val Pro Ser Ser Pro Gly Gln Glu Leu
200 205 210

Cys Gly Asn Asn Asn Val Thr Tyr Ile Ser Ser Cys His Met Arg
215 220 225

Gln Ala Thr Cys Phe Leu Gly Arg Ser Ile Gly Val Arg His Ala
230 235 240

Gly Ser Cys Ala Gly Thr Pro Glu Glu Pro Pro Gly Gly Glu Ser
245 250 255

Ala Glu Glu Glu Glu Asn Phe Val
260

<210> 42
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 42
tcctgtgagc acgtggtgtg 20

<210> 43
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 43
gggtgggata gacctgcg 18

<210> 44
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 44
aaggccaaga aggctgcc 18

<210> 45
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 45
ccaggcctgc agacccag 18

<210> 46
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 46
cttcctcagt ccttccagga tatc 24

<210> 47
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 47
aagctggata tcctccgtgt tgtc 24

<210> 48
<211> 27
<212> DNA

<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 48
cctgaagagg catgactgct tttctca 27

<210> 49
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 49
ggggataaac ctattaatta ttgctac 27

<210> 50
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 50
aacgtcacct acatctcctc gtgccacatg cgccaggcca cctg 44

<210> 51
<211> 1690
<212> DNA
<213> Homo Sapien

<400> 51
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cgctgctggg gttgtggctg ttgctgtgca gctgcggatg ccccgagggc 100

gccgagctgc gtgctccgcc agataaaatc gcgattattg gagccggaat 150

tggtggcact tcagcagcct attacctgcg gcagaaattt gggaaagatg 200

tgaagataga cctgtttgaa agagaagagg tcgggggccg cctggctacc 250

atgatggtgc aggggcaaga atacgaggca ggaggttctg tcatccatcc 300

tttaaatctg cacatgaaac gttttgtcaa agacctgggt ctctctgctg 350

ttcaggcctc tggtggccta ctggggatat ataatggaga gactctggta 400

tttgaggaga gcaactggtt cataattaac gtgattaaat tagtttggcg 450

ctatggattt caatccctcc gtatgcacat gtgggtagag gacgtgttag 500

acaagttcat gaggatctac cgctaccagt ctcatgacta tgccttcagt 550

agtgtcgaaa aattacttca tgctctagga ggagatgact tccttggaat 600

gcttaatcga acacttcttg aaaccttgca aaaggccggc ttttctgaga 650

agttcctcaa tgaaatgatt gctcctgtta tgagggtcaa ttatggccaa 700

agcacggaca tcaatgcctt tgtgggggcg gtgtcactgt cctgttctga 750

ttctggcctt tgggcagtag aaggtggcaa taaacttgtt tgctcagggc 800

ttctgcaggc atccaaaagc aatcttatat ctggctcagt aatgtacatc 850

gaggagaaaa caaagaccaa gtacacagga aatccaacaa agatgtatga 900

agtggtctac caaattggaa ctgagactcg ttcagacttc tatgacatcg 950

tcttggtggc cactccgttg aatcgaaaaa tgtcgaatat tacttttctc 1000

aactttgatc ctccaattga ggaattccat caatattatc aacatatagt 1050

gacaacttta gttaaggggg aattgaatac atctatcttt agctctagac 1100

ccatagataa atttggcctt aatacagttt taaccactga taattcagat 1150

ttgttcatta acagtattgg gattgtgccc tctgtgagag aaaaggaaga 1200

tcctgagcca tcaacagatg gaacatatgt ttggaagatc ttttcccaag 1250

aaactcttac taaagcacaa attttaaagc tctttctgtc ctatgattat 1300

gctgtgaaga agccatggct tgcatatcct cactataagc ccccggagaa 1350

atgcccctct atcattctcc atgatcgact ttattacctc aatggcatag 1400

agtgtgcagc aagtgccatg gagatgagtg ccattgcagc ccacaacgct 1450

gcactccttg cctatcaccg ctggaacggg cacacagaca tgattgatca 1500

ggatggctta tatgagaaac ttaaaactga actatgaagt gacacactcc 1550

tttttccccc cctagttcca aatgactatc agtggcaaaa aagaacaaaa 1600

tctgagcaga gatgattttg aaccagatat tttgccatta tcattgttta 1650

ataaaagtaa tccctgctgg tcataggaaa aaaaaaaaaa 1690

<210> 52
<211> 505
<212> PRT
<213> Homo Sapien

<400> 52

Met	Gly	Arg	Val	Val	Ala	Glu	Leu	Val	Ser	Ser	Leu	Leu	Gly	Leu
1				5				10						15

Trp	Leu	Leu	Leu	Cys	Ser	Cys	Gly	Cys	Pro	Glu	Gly	Ala	Glu	Leu
				20					25					30

Arg Ala Pro Pro Asp Lys Ile Ala Ile Ile Gly Ala Gly Ile Gly
35 40 45

Gly Thr Ser Ala Ala Tyr Tyr Leu Arg Gln Lys Phe Gly Lys Asp
50 55 60

Val Lys Ile Asp Leu Phe Glu Arg Glu Glu Val Gly Gly Arg Leu
65 70 75

Ala Thr Met Met Val Gln Gly Gln Glu Tyr Glu Ala Gly Gly Ser
80 85 90

Val Ile His Pro Leu Asn Leu His Met Lys Arg Phe Val Lys Asp
95 100 105

Leu Gly Leu Ser Ala Val Gln Ala Ser Gly Gly Leu Leu Gly Ile
110 115 120

Tyr Asn Gly Glu Thr Leu Val Phe Glu Glu Ser Asn Trp Phe Ile
125 130 135

Ile Asn Val Ile Lys Leu Val Trp Arg Tyr Gly Phe Gln Ser Leu
140 145 150

Arg Met His Met Trp Val Glu Asp Val Leu Asp Lys Phe Met Arg
155 160 165

Ile Tyr Arg Tyr Gln Ser His Asp Tyr Ala Phe Ser Ser Val Glu
170 175 180

Lys Leu Leu His Ala Leu Gly Gly Asp Asp Phe Leu Gly Met Leu
185 190 195

Asn Arg Thr Leu Leu Glu Thr Leu Gln Lys Ala Gly Phe Ser Glu
200 205 210

Lys Phe Leu Asn Glu Met Ile Ala Pro Val Met Arg Val Asn Tyr
215 220 225

Gly Gln Ser Thr Asp Ile Asn Ala Phe Val Gly Ala Val Ser Leu
230 235 240

Ser Cys Ser Asp Ser Gly Leu Trp Ala Val Glu Gly Gly Asn Lys
245 250 255

Leu Val Cys Ser Gly Leu Leu Gln Ala Ser Lys Ser Asn Leu Ile
260 265 270

Ser Gly Ser Val Met Tyr Ile Glu Glu Lys Thr Lys Thr Lys Tyr
275 280 285

Thr Gly Asn Pro Thr Lys Met Tyr Glu Val Val Tyr Gln Ile Gly
290 295 300

Thr Glu Thr Arg Ser Asp Phe Tyr Asp Ile Val Leu Val Ala Thr
305 310 315

Pro Leu Asn Arg Lys Met Ser Asn Ile Thr Phe Leu Asn Phe Asp

320 325 330

Pro Pro Ile Glu Glu Phe His Gln Tyr Tyr Gln His Ile Val Thr
335 340 345

Thr Leu Val Lys Gly Glu Leu Asn Thr Ser Ile Phe Ser Ser Arg
350 355 360

Pro Ile Asp Lys Phe Gly Leu Asn Thr Val Leu Thr Thr Asp Asn
365 370 375

Ser Asp Leu Phe Ile Asn Ser Ile Gly Ile Val Pro Ser Val Arg
380 385 390

Glu Lys Glu Asp Pro Glu Pro Ser Thr Asp Gly Thr Tyr Val Trp
395 400 405

Lys Ile Phe Ser Gln Glu Thr Leu Thr Lys Ala Gln Ile Leu Lys
410 415 420

Leu Phe Leu Ser Tyr Asp Tyr Ala Val Lys Lys Pro Trp Leu Ala
425 430 435

Tyr Pro His Tyr Lys Pro Pro Glu Lys Cys Pro Ser Ile Ile Leu
440 445 450

His Asp Arg Leu Tyr Tyr Leu Asn Gly Ile Glu Cys Ala Ala Ser
455 460 465

Ala Met Glu Met Ser Ala Ile Ala Ala His Asn Ala Ala Leu Leu
470 475 480

Ala Tyr His Arg Trp Asn Gly His Thr Asp Met Ile Asp Gln Asp
485 490 495

Gly Leu Tyr Glu Lys Leu Lys Thr Glu Leu
500 505

<210> 53
<211> 728
<212> DNA
<213> Homo Sapien

<400> 53
catttccaac aagagcactg gccaagtcag cttcttctga gagagtctct 50

agaagacatg atgctacact cagctttggg tctctgcctc ttactcgtca 100

cagtttcttc caaccttgcc attgcaataa aaaaggaaaa gaggcctcct 150

cagacactct caagaggatg ggagatgac atcacttggg tacaaactta 200

tgaagaaggt ctcttttatg ctcaaaaaag taagaagcca ttaatggtta 250

ttcatcacct ggaggattgt caatactctc aagcactaaa gaaagtattt 300

gcccaaaatg aagaaataca agaaatggct cagaataagt tcatcatgct 350

aaaccttatg catgaaacca ctgataagaa tttatcacct gatgggcaat 400

atgtgcctag aatcatgttt gtagaccctt ctttaacagt tagagctgac 450

atagctggaa gatactctaa cagattgtac acatatgagc ctcgggattt 500

acccctattg atagaaaaca tgaagaaagc attaagactt attcagtcag 550

agctataaga gatgatggaa aaaagccttc acttcaaaga agtcaaattt 600

catgaagaaa acctctggca cattgacaaa tactaaatgt gcaagtatat 650

agattttgta atattactat ttagtttttt taatgtgttt gcaatagtct 700

tattaaaata aatgtttttt aaatctga 728

<210> 54
<211> 166
<212> PRT
<213> Homo Sapien

<400> 54

Met	Met	Leu	His	Ser	Ala	Leu	Gly	Leu	Cys	Leu	Leu	Leu	Val	Thr	
1				5					10						15
Val	Ser	Ser	Asn	Leu	Ala	Ile	Ala	Ile	Lys	Lys	Glu	Lys	Arg	Pro	
				20					25						30
Pro	Gln	Thr	Leu	Ser	Arg	Gly	Trp	Gly	Asp	Asp	Ile	Thr	Trp	Val	
				35					40						45
Gln	Thr	Tyr	Glu	Glu	Gly	Leu	Phe	Tyr	Ala	Gln	Lys	Ser	Lys	Lys	
				50					55						60
Pro	Leu	Met	Val	Ile	His	His	Leu	Glu	Asp	Cys	Gln	Tyr	Ser	Gln	
				65					70						75
Ala	Leu	Lys	Lys	Val	Phe	Ala	Gln	Asn	Glu	Glu	Ile	Gln	Glu	Met	
				80					85						90
Ala	Gln	Asn	Lys	Phe	Ile	Met	Leu	Asn	Leu	Met	His	Glu	Thr	Thr	
				95					100						105
Asp	Lys	Asn	Leu	Ser	Pro	Asp	Gly	Gln	Tyr	Val	Pro	Arg	Ile	Met	
				110					115						120
Phe	Val	Asp	Pro	Ser	Leu	Thr	Val	Arg	Ala	Asp	Ile	Ala	Gly	Arg	
				125					130						135
Tyr	Ser	Asn	Arg	Leu	Tyr	Thr	Tyr	Glu	Pro	Arg	Asp	Leu	Pro	Leu	
				140					145						150
Leu	Ile	Glu	Asn	Met	Lys	Lys	Ala	Leu	Arg	Leu	Ile	Gln	Ser	Glu	
				155					160						165

Leu

<210> 55
<211> 537
<212> DNA
<213> Homo Sapien

<400> 55
taaaacagct acaatattcc agggccagtc acttgccatt tctcataaca 50

gcgtcagaga gaaagaactg actgaaacgt ttgagatgaa gaaagttctc 100

ctcctgatca cagccatctt ggcagtggct gttggtttcc cagtctctca 150

agaccaggaa cgagaaaaaa gaagtatcag tgacagcgat gaattagctt 200

cagggttttt tgtgttccct tacccatatc catttcgccc acttccacca 250

attccatttc caagatttcc atggtttaga cgtaattttc ctattccaat 300

acctgaatct gcccctacaa ctccccttcc tagcgaaaag taaacaagaa 350

ggataagtca cgataaacct ggtcacctga aattgaaatt gagccacttc 400

cttgaagaat caaaattcct gttaataaaa gaaaaacaaa tgtaattgaa 450

atagcacaca gcattctcta gtcaatatct ttagtgatct tctttaataa 500

acatgaaagc aaagattttg gtttcttaat ttccaca 537

<210> 56
<211> 85
<212> PRT
<213> Homo Sapien

<400> 56
Met Lys Lys Val Leu Leu Leu Ile Thr Ala Ile Leu Ala Val Ala
1 5 10 15

Val Gly Phe Pro Val Ser Gln Asp Gln Glu Arg Glu Lys Arg Ser
20 25 30

Ile Ser Asp Ser Asp Glu Leu Ala Ser Gly Phe Phe Val Phe Pro
35 40 45

Tyr Pro Tyr Pro Phe Arg Pro Leu Pro Pro Ile Pro Phe Pro Arg
50 55 60

Phe Pro Trp Phe Arg Arg Asn Phe Pro Ile Pro Ile Pro Glu Ser
65 70 75

Ala Pro Thr Thr Pro Leu Pro Ser Glu Lys
80 85

<210> 57
<211> 2997
<212> DNA
<213> Homo Sapien

<400> 57

cggacgcgtg ggcgggcgcg ccgggaggga ccggcggcgg catgggccgg 50

gggccctggg atgcgggccc gtctcgccgc ctgctgccgc tgttgctgct 100

gctcggcctg gcccgcggcg ccgcgggagc gccgggcccc gacggtttag 150

acgtctgtgc cacttgccat gaacatgcca catgccagca aagagaaggg 200

aagaagatct gtatttgcaa ctatggattt gtagggaacg ggaggactca 250

gtgtgttgat aaaaatgagt gccagtttgg agccactctt gtctgtggga 300

accacacatc ttgccacaac acccccgggg gcttctattg catttgcctg 350

gaaggatatc gagccacaaa caacaacaag acattcattc ccaacgatgg 400

caccttttgt acagacatag atgagtgtga agtttctggc ctgtgcaggc 450

atggagggcg atgcgtgaac actcatggga gctttgaatg ctactgtatg 500

gatggatact tgccaaggaa tggacctgaa cctttccacc cgaccaccga 550

tgccacatca tgcacagaaa tagactgtgg taccccctcct gaggttccag 600

atggctatat cataggaaat tatacgtcta gtctgggcag ccaggttcgt 650

tatgcttgca gagaaggatt cttcagtgtt ccagaagata cagtttcaag 700

ctgcacaggc ctgggcacat gggagtcccc aaaattacat tgccaagaga 750

tcaactgtgg caaccctcca gaaatgcggc acgccatctt ggtaggaaat 800

cacagctcca ggctgggcgg tgtggctcgc tatgtctgtc aagagggctt 850

tgagagccct ggaggaaaga tcacttctgt ttgcacagag aaaggcacct 900

ggagagaaag tactttaaca tgcacagaaa ttctgacaaa gattaatgat 950

gtatcactgt ttaatgatac ctgtgtgaga tggcaaataa actcaagaag 1000

aataaacccc aagatctcat atgtgatatc cataaaagga caacggttgg 1050

accctatgga atcagttcgt gaggagacag tcaacttgac cacagacagc 1100

aggaccccag aagtgtgcct agccctgtac ccaggcacca actacaccgt 1150

gaacatctcc acagcacctc ccaggcgctc gatgccagcc gtcatcggtt 1200

tccagacagc tgaagttgat ctcttagaag atgatggaag tttcaatatt 1250

tcaatattta atgaaacttg tttgaaattg aacaggcgtt ctaggaaagt 1300

tggatcagaa cacatgtacc aatttaccgt tctgggtcag aggtggtatc 1350

tggctaactt ttctcatgca acatcgttta acttcacaac gagggaacaa 1400

gtgcctgtag tgtgtttgga tctgtaccct acgactgatt atacggtgaa 1450

tgtgaccctg ctgagatctc ctaagcggca ctcagtgcaa ataacaatag 1500

caactccccc agcagtaaaa cagaccatca gtaacatttc aggatttaat 1550

gaaacctgct tgagatggag aagcatcaag acagctgata tggaggagat 1600

gtatttattc cacatttggg gccagagatg gtatcagaag gaatttgccc 1650

aggaaatgac ctttaatatc agtagcagca gccgagatcc cgaggtgtgc 1700

ttggacctac gtccgggtac caactacaat gtcagtctcc gggctctgtc 1750

ttcggaactt cctgtggtca tctccctgac aacccagata acagagcctc 1800

ccctcccgga agtagaattt tttacggtgc acagaggacc tctaccacgc 1850

ctcagactga ggaaagccaa ggagaaaaat ggaccaatca gttcatatca 1900

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aaggcgcttc ctccttcttt agcaacgcct ctgatgctga tggatacgtg 2000

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ggctatccct gaggagtcac cataaggaga aaactcagga attctgagtc 2500

ttccctgcta caggaccagt tctgtgcaat gaacttgaga ctcctgatgt 2550

acactgtgat attgaccgaa ggctacatac agatctgtga atcttggctg 2600

ggacttcctc tgagtgatgc ctgagggtca gctcctctag acattgactg 2650

caagagaatc tctgcaacct cctatataaa agcatttctg ttaattcatt 2700

cagaatccat tctttacaat atgcagtgag atgggcttaa gtttgggcta 2750

gagtttgact ttatgaagga ggtcattgaa aaagagaaca gtgacgtagg 2800

caaatgtttc aagcacttta gaaacagtac ttttcctata attagttgat 2850

atactaatga gaaaatatac tagcctggcc atgccaataa gtttcctgct 2900

gtgtctgtta ggcagcattg ctttgatgca atttctattg tcctatatat 2950

tcaaaagtaa tgtctacatt ccagtaaaaa tatcccgtaa ttaaaaa 2997

<210> 58
<211> 747
<212> PRT
<213> Homo Sapien

<400> 58

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Met Gly Arg Gly Pro Trp Asp Ala Gly Pro Ser Arg Arg Leu Leu
  1               5                  10                  15

Pro Leu Leu Leu Leu Leu Gly Leu Ala Arg Gly Ala Ala Gly Ala
             20                  25                  30

Pro Gly Pro Asp Gly Leu Asp Val Cys Ala Thr Cys His Glu His
         35                  40                  45

Ala Thr Cys Gln Gln Arg Glu Gly Lys Lys Ile Cys Ile Cys Asn
     50                  55                  60

Tyr Gly Phe Val Gly Asn Gly Arg Thr Gln Cys Val Asp Lys Asn
 65                  70                  75

Glu Cys Gln Phe Gly Ala Thr Leu Val Cys Gly Asn His Thr Ser
             80                  85                  90

Cys His Asn Thr Pro Gly Gly Phe Tyr Cys Ile Cys Leu Glu Gly
         95                 100                 105

Tyr Arg Ala Thr Asn Asn Asn Lys Thr Phe Ile Pro Asn Asp Gly
    110                 115                 120

Thr Phe Cys Thr Asp Ile Asp Glu Cys Glu Val Ser Gly Leu Cys
125                 130                 135

Arg His Gly Gly Arg Cys Val Asn Thr His Gly Ser Phe Glu Cys
            140                 145                 150

Tyr Cys Met Asp Gly Tyr Leu Pro Arg Asn Gly Pro Glu Pro Phe
        155                 160                 165

His Pro Thr Thr Asp Ala Thr Ser Cys Thr Glu Ile Asp Cys Gly
    170                 175                 180

Thr Pro Pro Glu Val Pro Asp Gly Tyr Ile Ile Gly Asn Tyr Thr
185                 190                 195

Ser Ser Leu Gly Ser Gln Val Arg Tyr Ala Cys Arg Glu Gly Phe
            200                 205                 210

Phe Ser Val Pro Glu Asp Thr Val Ser Ser Cys Thr Gly Leu Gly
        215                 220                 225

Thr Trp Glu Ser Pro Lys Leu His Cys Gln Glu Ile Asn Cys Gly
    230                 235                 240
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Asn Pro Pro Glu Met Arg His Ala Ile Leu Val Gly Asn His Ser
                245                 250                 255

Ser Arg Leu Gly Gly Val Ala Arg Tyr Val Cys Gln Glu Gly Phe
            260                 265                 270

Glu Ser Pro Gly Gly Lys Ile Thr Ser Val Cys Thr Glu Lys Gly
        275                 280                 285

Thr Trp Arg Glu Ser Thr Leu Thr Cys Thr Glu Ile Leu Thr Lys
    290                 295                 300

Ile Asn Asp Val Ser Leu Phe Asn Asp Thr Cys Val Arg Trp Gln
305                 310                 315

Ile Asn Ser Arg Arg Ile Asn Pro Lys Ile Ser Tyr Val Ile Ser
            320                 325                 330

Ile Lys Gly Gln Arg Leu Asp Pro Met Glu Ser Val Arg Glu Glu
        335                 340                 345

Thr Val Asn Leu Thr Thr Asp Ser Arg Thr Pro Glu Val Cys Leu
    350                 355                 360

Ala Leu Tyr Pro Gly Thr Asn Tyr Thr Val Asn Ile Ser Thr Ala
365                 370                 375

Pro Pro Arg Arg Ser Met Pro Ala Val Ile Gly Phe Gln Thr Ala
            380                 385                 390

Glu Val Asp Leu Leu Glu Asp Asp Gly Ser Phe Asn Ile Ser Ile
        395                 400                 405

Phe Asn Glu Thr Cys Leu Lys Leu Asn Arg Arg Ser Arg Lys Val
    410                 415                 420

Gly Ser Glu His Met Tyr Gln Phe Thr Val Leu Gly Gln Arg Trp
425                 430                 435

Tyr Leu Ala Asn Phe Ser His Ala Thr Ser Phe Asn Phe Thr Thr
            440                 445                 450

Arg Glu Gln Val Pro Val Val Cys Leu Asp Leu Tyr Pro Thr Thr
        455                 460                 465

Asp Tyr Thr Val Asn Val Thr Leu Leu Arg Ser Pro Lys Arg His
    470                 475                 480

Ser Val Gln Ile Thr Ile Ala Thr Pro Pro Ala Val Lys Gln Thr
485                 490                 495

Ile Ser Asn Ile Ser Gly Phe Asn Glu Thr Cys Leu Arg Trp Arg
            500                 505                 510

Ser Ile Lys Thr Ala Asp Met Glu Glu Met Tyr Leu Phe His Ile
        515                 520                 525

Trp Gly Gln Arg Trp Tyr Gln Lys Glu Phe Ala Gln Glu Met Thr
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530 535 540

Phe Asn Ile Ser Ser Ser Ser Arg Asp Pro Glu Val Cys Leu Asp
545 550 555

Leu Arg Pro Gly Thr Asn Tyr Asn Val Ser Leu Arg Ala Leu Ser
560 565 570

Ser Glu Leu Pro Val Val Ile Ser Leu Thr Thr Gln Ile Thr Glu
575 580 585

Pro Pro Leu Pro Glu Val Glu Phe Phe Thr Val His Arg Gly Pro
590 595 600

Leu Pro Arg Leu Arg Leu Arg Lys Ala Lys Glu Lys Asn Gly Pro
605 610 615

Ile Ser Ser Tyr Gln Val Leu Val Leu Pro Leu Ala Leu Gln Ser
620 625 630

Thr Phe Ser Cys Asp Ser Glu Gly Ala Ser Ser Phe Phe Ser Asn
635 640 645

Ala Ser Asp Ala Asp Gly Tyr Val Ala Ala Glu Leu Leu Ala Lys
650 655 660

Asp Val Pro Asp Asp Ala Met Glu Ile Pro Ile Gly Asp Arg Leu
665 670 675

Tyr Tyr Gly Glu Tyr Tyr Asn Ala Pro Leu Lys Arg Gly Ser Asp
680 685 690

Tyr Cys Ile Ile Leu Arg Ile Thr Ser Glu Trp Asn Lys Val Arg
695 700 705

Arg His Ser Cys Ala Val Trp Ala Gln Val Lys Asp Ser Ser Leu
710 715 720

Met Leu Leu Gln Met Ala Gly Val Gly Leu Gly Ser Leu Ala Val
725 730 735

Val Ile Ile Leu Thr Phe Leu Ser Phe Ser Ala Val
740 745

<210> 59
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 59
ccacttgcca tgaacatgcc ac 22

<210> 60
<211> 25
<212> DNA

<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 60
cctcttgaca gacatagcga gccac 25

<210> 61
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 61
cactcttgtc tgtgggaacc acacatcttg ccacaactgt ggc 43

<210> 62
<211> 2015
<212> DNA
<213> Homo Sapien

<400> 62
ggaaaaggta cccgcgagag acagccagca gttctgtgga gcagcggtgg 50

ccggctagga tgggctgtct ctggggtctg gctctgcccc ttttcttctt 100

ctgctgggag gttggggtct ctgggagctc tgcaggcccc agcacccgca 150

gagcagacac tgcgatgaca acggacgaca cagaagtgcc cgctatgact 200

ctagcaccgg gccacgccgc tctggaaact caaacgctga gcgctgagac 250

ctcttctagg gcctcaaccc cagccggccc cattccagaa gcagagacca 300

ggggagccaa gagaatttcc cctgcaagag agaccaggag tttcacaaaa 350

acatctccca acttcatggt gctgatcgcc acctccgtgg agacatcagc 400

cgccagtggc agccccgagg gagctggaat gaccacagtt cagaccatca 450

caggcagtga tcccgaggaa gccatctttg acaccctttg caccgatgac 500

agctctgaag aggcaaagac actcacaatg gacatattga cattggctca 550

cacctccaca gaagctaagg gcctgtcctc agagagcagt gcctcttccg 600

acggccccca tccagtcatc accccgtcac gggcctcaga gagcagcgcc 650

tcttccgacg gcccccatcc agtcatcacc ccgtcacggg cctcagagag 700

cagcgcctct tccgacggcc cccatccagt catcaccccg tcatggtccc 750

cgggatctga tgtcactctc ctcgctgaag ccctggtgac tgtcacaaac 800

atcgaggtta ttaattgcag catcacagaa atagaaacaa caacttccag 850

catccctggg gcctcagaca tagatctcat ccccacggaa ggggtgaagg 900

cctcgtccac ctccgatcca ccagctctgc ctgactccac tgaagcaaaa 950

ccacacatca ctgaggtcac agcctctgcc gagaccctgt ccacagccgg 1000

caccacagag tcagctgcac ctcatgccac ggttgggacc ccactcccca 1050

ctaacagcgc cacagaaaga gaagtgacag cacccggggc cacgaccctc 1100

agtggagctc tggtcacagt tagcaggaat cccctggaag aaacctcagc 1150

cctctctgtt gagacaccaa gttacgtcaa agtctcagga gcagctccgg 1200

tctccataga ggctgggtca gcagtgggca aaacaacttc ctttgctggg 1250

agctctgctt cctcctacag cccctcggaa gccgccctca agaacttcac 1300

cccttcagag acaccgacca tggacatcgc aaccaagggg cccttcccca 1350

ccagcaggga ccctcttcct tctgtccctc cgactacaac caacagcagc 1400

cgagggacga acagcacctt agccaagatc acaacctcag cgaagaccac 1450

gatgaagccc caacagccac gcccacgact gcccggacga ggccgaccac 1500

agacgtgagt gcaggtgaaa atggaggttt cctcctcctg cggctgagtg 1550

tggcttcccc ggaagacctc actgacccca gagtggcaga aaggctgatg 1600

cagcagctcc accgggaact ccacgcccac gcgcctcact tccaggtctc 1650

cttactgcgt gtcaggagag gctaacggac atcagctgca gccaggcatg 1700

tcccgtatgc caaaagaggg tgctgcccct agcctgggcc cccaccgaca 1750

gactgcagct gcgttactgt gctgagaggt acccagaagg ttcccatgaa 1800

gggcagcatg tccaagcccc taaccccaga tgtggcaaca ggaccctcgc 1850

tcacatccac cggagtgtat gtatggggag gggcttcacc tgttcccaga 1900

ggtgtccttg gactcacctt ggcacatgtt ctgtgtttca gtaaagagag 1950

acctgatcac ccatctgtgt gcttccatcc tgcattaaaa ttcactcagt 2000

gtggcccaaa aaaaa 2015

<210> 63
<211> 482
<212> PRT
<213> Homo Sapien

<400> 63
Met Gly Cys Leu Trp Gly Leu Ala Leu Pro Leu Phe Phe Phe Cys
1 5 10 15

Trp Glu Val Gly Val Ser Gly Ser Ser Ala Gly Pro Ser Thr Arg

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                  20                  25                  30

Arg Ala Asp Thr Ala Met Thr Thr Asp Asp Thr Glu Val Pro Ala
                  35                  40                  45

Met Thr Leu Ala Pro Gly His Ala Ala Leu Glu Thr Gln Thr Leu
                  50                  55                  60

Ser Ala Glu Thr Ser Ser Arg Ala Ser Thr Pro Ala Gly Pro Ile
                  65                  70                  75

Pro Glu Ala Glu Thr Arg Gly Ala Lys Arg Ile Ser Pro Ala Arg
                  80                  85                  90

Glu Thr Arg Ser Phe Thr Lys Thr Ser Pro Asn Phe Met Val Leu
                  95                 100                 105

Ile Ala Thr Ser Val Glu Thr Ser Ala Ala Ser Gly Ser Pro Glu
                 110                 115                 120

Gly Ala Gly Met Thr Thr Val Gln Thr Ile Thr Gly Ser Asp Pro
                 125                 130                 135

Glu Glu Ala Ile Phe Asp Thr Leu Cys Thr Asp Asp Ser Ser Glu
                 140                 145                 150

Glu Ala Lys Thr Leu Thr Met Asp Ile Leu Thr Leu Ala His Thr
                 155                 160                 165

Ser Thr Glu Ala Lys Gly Leu Ser Ser Glu Ser Ser Ala Ser Ser
                 170                 175                 180

Asp Gly Pro His Pro Val Ile Thr Pro Ser Arg Ala Ser Glu Ser
                 185                 190                 195

Ser Ala Ser Ser Asp Gly Pro His Pro Val Ile Thr Pro Ser Arg
                 200                 205                 210

Ala Ser Glu Ser Ser Ala Ser Ser Asp Gly Pro His Pro Val Ile
                 215                 220                 225

Thr Pro Ser Trp Ser Pro Gly Ser Asp Val Thr Leu Leu Ala Glu
                 230                 235                 240

Ala Leu Val Thr Val Thr Asn Ile Glu Val Ile Asn Cys Ser Ile
                 245                 250                 255

Thr Glu Ile Glu Thr Thr Thr Ser Ser Ile Pro Gly Ala Ser Asp
                 260                 265                 270

Ile Asp Leu Ile Pro Thr Glu Gly Val Lys Ala Ser Ser Thr Ser
                 275                 280                 285

Asp Pro Pro Ala Leu Pro Asp Ser Thr Glu Ala Lys Pro His Ile
                 290                 295                 300

Thr Glu Val Thr Ala Ser Ala Glu Thr Leu Ser Thr Ala Gly Thr
                 305                 310                 315
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Thr Glu Ser Ala Ala Pro His Ala Thr Val Gly Thr Pro Leu Pro
320 325 330

Thr Asn Ser Ala Thr Glu Arg Glu Val Thr Ala Pro Gly Ala Thr
335 340 345

Thr Leu Ser Gly Ala Leu Val Thr Val Ser Arg Asn Pro Leu Glu
350 355 360

Glu Thr Ser Ala Leu Ser Val Glu Thr Pro Ser Tyr Val Lys Val
365 370 375

Ser Gly Ala Ala Pro Val Ser Ile Glu Ala Gly Ser Ala Val Gly
380 385 390

Lys Thr Thr Ser Phe Ala Gly Ser Ser Ala Ser Ser Tyr Ser Pro
395 400 405

Ser Glu Ala Ala Leu Lys Asn Phe Thr Pro Ser Glu Thr Pro Thr
410 415 420

Met Asp Ile Ala Thr Lys Gly Pro Phe Pro Thr Ser Arg Asp Pro
425 430 435

Leu Pro Ser Val Pro Pro Thr Thr Thr Asn Ser Ser Arg Gly Thr
440 445 450

Asn Ser Thr Leu Ala Lys Ile Thr Thr Ser Ala Lys Thr Thr Met
455 460 465

Lys Pro Gln Gln Pro Arg Pro Arg Leu Pro Gly Arg Gly Arg Pro
470 475 480

Gln Thr

<210> 64
<211> 1252
<212> DNA
<213> Homo Sapien

<400> 64
gcctctgaat tgttgggcag tctggcagtg gagctctccc cggtctgaca 50

gccactccag aggccatgct tcgtttcttg ccagatttgg ctttcagctt 100

cctgttaatt ctggctttgg gccaggcagt ccaatttcaa gaatatgtct 150

ttctccaatt tctgggctta gataaggcgc cttcacccca gaagttccaa 200

cctgtgcctt atatcttgaa gaaaattttc caggatcgcg aggcagcagc 250

gaccactggg gtctcccgag acttatgcta cgtaaaggag ctgggcgtcc 300

gcgggaatgt acttcgcttt ctcccagacc aaggtttctt tctttaccca 350

aagaaaattt cccaagcttc ctcctgcctg cagaagctcc tctactttaa 400

cctgtctgcc atcaaagaaa gggaacagtt gacattggcc cagctgggcc 450

tggacttggg gcccaattct tactataacc tgggaccaga gctggaactg 500

gctctgttcc tggttcagga gcctcatgtg tggggccaga ccacccctaa 550

gccaggtaaa atgtttgtgt tgcggtcagt cccatggcca caaggtgctg 600

ttcacttcaa cctgctggat gtagctaagg attggaatga caaccccgg 650

aaaaatttcg ggttattcct ggagatactg gtcaaagaag atagagactc 700

aggggtgaat tttcagcctg aagacacctg tgccagacta agatgctccc 750

ttcatgcttc cctgctggtg gtgactctca accctgatca gtgccacccct 800

tctcggaaaa ggagagcagc catccctgtc cccaagcttt cttgtaagaa 850

cctctgccac cgtcaccagc tattcattaa cttccgggac ctgggttggc 900

acaagtggat cattgccccc aaggggttca tggcaaatta ctgccatgga 950

gagtgtccct tctcactgac catctctctc aacagctcca attatgcttt 1000

catgcaagcc ctgatgcatg ccgttgaccc agagatcccc caggctgtgt 1050

gtatccccac caagctgtct cccatttcca tgctctacca ggacaataat 1100

gacaatgtca ttctacgaca ttatgaagac atggtagtcg atgaatgtgg 1150

gtgtgggtag gatgtcagaa atgggaatag aaggagtgtt cttagggtaa 1200

atcttttaat aaaactacct atctggttta tgaccactta gatcgaaatg 1250

tc 1252

<210> 65
<211> 364
<212> PRT
<213> Homo Sapien

<400> 65
Met Leu Arg Phe Leu Pro Asp Leu Ala Phe Ser Phe Leu Leu Ile
1 5 10 15

Leu Ala Leu Gly Gln Ala Val Gln Phe Gln Glu Tyr Val Phe Leu
20 25 30

Gln Phe Leu Gly Leu Asp Lys Ala Pro Ser Pro Gln Lys Phe Gln
35 40 45

Pro Val Pro Tyr Ile Leu Lys Lys Ile Phe Gln Asp Arg Glu Ala
50 55 60

Ala Ala Thr Thr Gly Val Ser Arg Asp Leu Cys Tyr Val Lys Glu
65 70 75

Leu Gly Val Arg Gly Asn Val Leu Arg Phe Leu Pro Asp Gln Gly

```
                  80                  85                  90

Phe Phe Leu Tyr Pro Lys Lys Ile Ser Gln Ala Ser Ser Cys Leu
                  95                 100                 105

Gln Lys Leu Leu Tyr Phe Asn Leu Ser Ala Ile Lys Glu Arg Glu
                 110                 115                 120

Gln Leu Thr Leu Ala Gln Leu Gly Leu Asp Leu Gly Pro Asn Ser
                 125                 130                 135

Tyr Tyr Asn Leu Gly Pro Glu Leu Glu Leu Ala Leu Phe Leu Val
                 140                 145                 150

Gln Glu Pro His Val Trp Gly Gln Thr Thr Pro Lys Pro Gly Lys
                 155                 160                 165

Met Phe Val Leu Arg Ser Val Pro Trp Pro Gln Gly Ala Val His
                 170                 175                 180

Phe Asn Leu Leu Asp Val Ala Lys Asp Trp Asn Asp Asn Pro Arg
                 185                 190                 195

Lys Asn Phe Gly Leu Phe Leu Glu Ile Leu Val Lys Glu Asp Arg
                 200                 205                 210

Asp Ser Gly Val Asn Phe Gln Pro Glu Asp Thr Cys Ala Arg Leu
                 215                 220                 225

Arg Cys Ser Leu His Ala Ser Leu Leu Val Val Thr Leu Asn Pro
                 230                 235                 240

Asp Gln Cys His Pro Ser Arg Lys Arg Arg Ala Ala Ile Pro Val
                 245                 250                 255

Pro Lys Leu Ser Cys Lys Asn Leu Cys His Arg His Gln Leu Phe
                 260                 265                 270

Ile Asn Phe Arg Asp Leu Gly Trp His Lys Trp Ile Ile Ala Pro
                 275                 280                 285

Lys Gly Phe Met Ala Asn Tyr Cys His Gly Glu Cys Pro Phe Ser
                 290                 295                 300

Leu Thr Ile Ser Leu Asn Ser Ser Asn Tyr Ala Phe Met Gln Ala
                 305                 310                 315

Leu Met His Ala Val Asp Pro Glu Ile Pro Gln Ala Val Cys Ile
                 320                 325                 330

Pro Thr Lys Leu Ser Pro Ile Ser Met Leu Tyr Gln Asp Asn Asn
                 335                 340                 345

Asp Asn Val Ile Leu Arg His Tyr Glu Asp Met Val Val Asp Glu
                 350                 355                 360

Cys Gly Cys Gly
```

<210> 66
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 66
gtctgacagc cactccagag 20

<210> 67
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 67
tctccaattt ctgggcttag ataaggcgcc ttcaccccag aagttcc 47

<210> 68
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 68
gtcccaggtt atagtaagaa ttgg 24

<210> 69
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 69
gtgttgcggt cagtcccatg 20

<210> 70
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 70
gctgtctccc atttccatgc 20

<210> 71
<211> 24
<212> DNA

<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 71
cgactaccat gtcttcataa tgtc 24

<210> 72
<211> 2849
<212> DNA
<213> Homo Sapien

<400> 72
cactttctcc ctctcttcct ttactttcga gaaaccgcgc ttccgcttct 50

ggtcgcagag acctcggaga ccgcgccggg gagacggagg tgctgtgggt 100

ggggggggacc tgtggctgct cgtaccgccc cccaccctcc tcttctgcac 150

tgccgtcctc cggaagacct tttcccctgc tctgtttcct tcaccgagtc 200

tgtgcatcgc cccggacctg gccgggagga ggcttggccg gcgggagatg 250

ctctaggggc ggcgcgggag gagcggccgg cgggacggag ggcccggcag 300

gaagatgggc tcccgtggac agggactctt gctggcgtac tgcctgctcc 350

ttgcctttgc ctctggcctg gtcctgagtc gtgtgcccca tgtccagggg 400

gaacagcagg agtgggaggg gactgaggag ctgccgtcgc ctccggacca 450

tgccgagagg gctgaagaac aacatgaaaa atacaggccc agtcaggacc 500

aggggctccc tgcttcccgg tgcttgcgct gctgtgaccc cggtacctcc 550

atgtacccgg cgaccgccgt gccccagatc aacatcacta tcttgaaagg 600

ggagaagggt gaccgcggag atcgaggcct ccaagggaaa tatggcaaaa 650

caggctcagc aggggccagg ggccacactg gacccaaagg gcagaagggc 700

tccatggggg cccctgggga gcggtgcaag agccactacg ccgccttttc 750

ggtgggccgg aagaagccca tgcacagcaa ccactactac cagacggtga 800

tcttcgacac ggagttcgtg aacctctacg accacttcaa catgttcacc 850

ggcaagttct actgctacgt gcccggcctc tacttcttca gcctcaacgt 900

gcacacctgg aaccagaagg agacctacct gcacatcatg aagaacgagg 950

aggaggtggt gatcttgttc gcgcaggtgg gcgaccgcag catcatgcaa 1000

agccagagcc tgatgctgga gctgcgagag caggaccagg tgtgggtacg 1050

cctctacaag ggcgaacgtg agaacgccat cttcagcgag gagctggaca 1100

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gcattcagtg agacgccctg cacacacaga aagccaaagc gatcggtgct 1300

cccagatccc gcagcctctg gagagagctg acggcagatg aaatcaccag 1350

ggcggggcac ccgcgagaac cctctgggac cttccgcggc cctctctgca 1400

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cccagggtgc ggcaccgcgg ctccagtcct tggaaataat taggcaaatt 1500

ctaaaggtct caaaaggagc aaagtaaacc gtggaggaca aagaaaaggg 1550

ttgttatttt tgtctttcca gccagcctgc tggctcccaa gagagaggcc 1600

ttttcagttg agactctgct taagagaaga tccaaagtta aagctctggg 1650

gtcaggggag gggccggggg caggaaacta cctctggctt aattctttta 1700

agccacgtag gaactttctt gagggatagg tggaccctga catccctgtg 1750

gccttgccca agggctctgc tggtctttct gagtcacagc tgcgaggtga 1800

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tccctaagtc cctctcttta aagaacttct gcgggtcaga ctctgaagcc 2750

gagttgctgt gggcgtgccc ggaagcagag cgccacactc gctgcttaag 2800

ctccccccagc tctttccaga aaacattaaa ctcagaattg tgttttcaa 2849

<210> 73
<211> 281
<212> PRT
<213> Homo Sapien

<400> 73

Met	Gly	Ser	Arg	Gly	Gln	Gly	Leu	Leu	Leu	Ala	Tyr	Cys	Leu	Leu
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Leu	Ala	Phe	Ala	Ser	Gly	Leu	Val	Leu	Ser	Arg	Val	Pro	His	Val
				20				25						30
Gln	Gly	Glu	Gln	Gln	Glu	Trp	Glu	Gly	Thr	Glu	Glu	Leu	Pro	Ser
				35				40						45
Pro	Pro	Asp	His	Ala	Glu	Arg	Ala	Glu	Glu	Gln	His	Glu	Lys	Tyr
				50				55						60
Arg	Pro	Ser	Gln	Asp	Gln	Gly	Leu	Pro	Ala	Ser	Arg	Cys	Leu	Arg
				65				70						75
Cys	Cys	Asp	Pro	Gly	Thr	Ser	Met	Tyr	Pro	Ala	Thr	Ala	Val	Pro
				80				85						90
Gln	Ile	Asn	Ile	Thr	Ile	Leu	Lys	Gly	Glu	Lys	Gly	Asp	Arg	Gly
				95				100						105
Asp	Arg	Gly	Leu	Gln	Gly	Lys	Tyr	Gly	Lys	Thr	Gly	Ser	Ala	Gly
				110				115						120
Ala	Arg	Gly	His	Thr	Gly	Pro	Lys	Gly	Gln	Lys	Gly	Ser	Met	Gly
				125				130						135
Ala	Pro	Gly	Glu	Arg	Cys	Lys	Ser	His	Tyr	Ala	Ala	Phe	Ser	Val
				140				145						150
Gly	Arg	Lys	Lys	Pro	Met	His	Ser	Asn	His	Tyr	Tyr	Gln	Thr	Val
				155				160						165
Ile	Phe	Asp	Thr	Glu	Phe	Val	Asn	Leu	Tyr	Asp	His	Phe	Asn	Met
				170				175						180
Phe	Thr	Gly	Lys	Phe	Tyr	Cys	Tyr	Val	Pro	Gly	Leu	Tyr	Phe	Phe
				185				190						195
Ser	Leu	Asn	Val	His	Thr	Trp	Asn	Gln	Lys	Glu	Thr	Tyr	Leu	His

200 205 210

Ile Met Lys Asn Glu Glu Glu Val Val Ile Leu Phe Ala Gln Val
215 220 225

Gly Asp Arg Ser Ile Met Gln Ser Gln Ser Leu Met Leu Glu Leu
230 235 240

Arg Glu Gln Asp Gln Val Trp Val Arg Leu Tyr Lys Gly Glu Arg
245 250 255

Glu Asn Ala Ile Phe Ser Glu Glu Leu Asp Thr Tyr Ile Thr Phe
260 265 270

Ser Gly Tyr Leu Val Lys His Ala Thr Glu Pro
275 280

<210> 74
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 74
tacaggccca gtcaggacca gggg 24

<210> 75
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 75
ctgaagaagt agaggccggg cacg 24

<210> 76
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 76
cccggtgctt gcgctgctgt gacccccggta cctccatgta cccgg 45

<210> 77
<211> 1042
<212> DNA
<213> Homo Sapien

<400> 77
gaattcggca cgagggaaga agagaaagaa aatctccggg gctgctggga 50

gcatataaag aagccctgtg gccttgctgg ttttaccatc cagaccagag 100

tcaggccaca gacggacatg gctgctcaag gctggtccat gctcctgctg 150

gctgtcctta acctaggcat cttcgtccgt ccctgtgaca ctcaagagct 200

acgatgtctg tgtattcagg aacactctga attcattcct ctcaaactca 250

ttaaaaatat aatggtgata ttcgagacca tttactgcaa cagaaaggaa 300

gtgatagcag tcccaaaaaa tgggagtatg atttgtttgg atcctgatgc 350

tccatgggtg aaggctactg ttggcccaat tactaacagg ttcctacctg 400

aggacctcaa acaaaaggaa tttccaccgg caatgaagct tctgtatagt 450

gttgagcatg aaaagcctct atatctttca tttgggagac ctgagaacaa 500

gagaatattt ccctttccaa ttcgggagac ctctagacac tttgctgatt 550

tagctcacaa cagtgatagg aattttctac gggactccag tgaagtcagc 600

ttgacaggca gtgatgccta aaagccactc atgaggcaaa gagtttcaag 650

gaagctctcc tcctggagtt ttggcgttct cattcttata ctctattccc 700

gcgttagtct ggtgtatgga tctatgagct ctcttttaat attttattat 750

aaatgtttta tttacttaac ttcctagtga atgttcacag gtgactgctc 800

ccccatcccc atttcttgat attacatata atggcatcat ataccccttt 850

attgactgac aaactactca gattgcttaa cattttgtgc ttcaaagtct 900

tatcccactc cactatgggc tgttacagag tgcatctcgg tgtagagcaa 950

ggctccttgt cttcagtgcc ccagggtgaa atacttcttt gaaaaatttt 1000

cattcatcag aaaatctgaa ataaaaatat gtcttaattg ag 1042

<210> 78
<211> 167
<212> PRT
<213> Homo Sapien

<400> 78
Met Ala Ala Gln Gly Trp Ser Met Leu Leu Leu Ala Val Leu Asn
1 5 10 15

Leu Gly Ile Phe Val Arg Pro Cys Asp Thr Gln Glu Leu Arg Cys
20 25 30

Leu Cys Ile Gln Glu His Ser Glu Phe Ile Pro Leu Lys Leu Ile
35 40 45

Lys Asn Ile Met Val Ile Phe Glu Thr Ile Tyr Cys Asn Arg Lys
50 55 60

Glu Val Ile Ala Val Pro Lys Asn Gly Ser Met Ile Cys Leu Asp
65 70 75

Pro Asp Ala Pro Trp Val Lys Ala Thr Val Gly Pro Ile Thr Asn
80 85 90

Arg Phe Leu Pro Glu Asp Leu Lys Gln Lys Glu Phe Pro Pro Ala
95 100 105

Met Lys Leu Leu Tyr Ser Val Glu His Glu Lys Pro Leu Tyr Leu
110 115 120

Ser Phe Gly Arg Pro Glu Asn Lys Arg Ile Phe Pro Phe Pro Ile
125 130 135

Arg Glu Thr Ser Arg His Phe Ala Asp Leu Ala His Asn Ser Asp
140 145 150

Arg Asn Phe Leu Arg Asp Ser Ser Glu Val Ser Leu Thr Gly Ser
155 160 165

Asp Ala

<210> 79
<211> 798
<212> DNA
<213> Homo Sapien

<220>
<221> unsure
<222> 794
<223> unknown base

<400> 79
cagacatggc tcagtcactg gctctgagcc tccttatcct ggttctggcc 50

tttggcatcc ccaggaccca aggcagtgat ggaggggctc aggactgttg 100

cctcaagtac agccaaagga agattcccgc caaggttgtc cgcagctacc 150

ggaagcagga accaagctta ggctgctcca tcccagctat cctgttcttg 200

ccccgcaagc gctctcaggc agagctatgt gcagacccaa aggagctctg 250

ggtgcagcag ctgatgcagc atctggacaa gacaccatcc ccacagaaac 300

cagcccaggg ctgcaggaag gacagggggg cctccaagac tggcaagaaa 350

ggaaagggct ccaaaggctg caagaggact gagcggtcac agacccctaa 400

agggccatag cccagtgagc agcctggagc cctggagacc ccaccagcct 450

caccagcgct tgaagcctga acccaagatg caagaaggag gctatgctca 500

ggggccctgg agcagccacc ccatgctggc cttgccacac tctttctcct 550

gctttaacca ccccatctgc attcccagct ctaccctgca tggctgagct 600

gcccacagca ggccaggtcc agagagaccg aggagggaga gtctcccagg 650

gagcatgaga ggaggcagca ggactgtccc cttgaaggag aatcatcagg 700

accctggacc tgatacggct ccccagtaca ccccacctct tccttgtaaa 750

tatgatttat acctaactga ataaaaagct gttctgtctt cccnccca 798

<210> 80
<211> 134
<212> PRT
<213> Homo Sapien

<400> 80

Met	Ala	Gln	Ser	Leu	Ala	Leu	Ser	Leu	Leu	Ile	Leu	Val	Leu	Ala	
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Phe	Gly	Ile	Pro	Arg	Thr	Gln	Gly	Ser	Asp	Gly	Gly	Ala	Gln	Asp	
				20				25						30	
Cys	Cys	Leu	Lys	Tyr	Ser	Gln	Arg	Lys	Ile	Pro	Ala	Lys	Val	Val	
				35				40						45	
Arg	Ser	Tyr	Arg	Lys	Gln	Glu	Pro	Ser	Leu	Gly	Cys	Ser	Ile	Pro	
				50				55						60	
Ala	Ile	Leu	Phe	Leu	Pro	Arg	Lys	Arg	Ser	Gln	Ala	Glu	Leu	Cys	
				65				70						75	
Ala	Asp	Pro	Lys	Glu	Leu	Trp	Val	Gln	Gln	Leu	Met	Gln	His	Leu	
				80				85						90	
Asp	Lys	Thr	Pro	Ser	Pro	Gln	Lys	Pro	Ala	Gln	Gly	Cys	Arg	Lys	
				95				100						105	
Asp	Arg	Gly	Ala	Ser	Lys	Thr	Gly	Lys	Lys	Gly	Lys	Gly	Ser	Lys	
				110				115						120	
Gly	Cys	Lys	Arg	Thr	Glu	Arg	Ser	Gln	Thr	Pro	Lys	Gly	Pro		
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<210> 81
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 81
agacatggct cagtcactgg 20

<210> 82
<211> 19
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 82
gacccctaaa gggccatag 19

<210> 83
<211> 924
<212> DNA
<213> Homo Sapien

<400> 83
aaggagcagc ccgcaagcac caagtgagag gcatgaagtt acagtgtgtt 50

tccctttggc tcctgggtac aatactgata ttgtgctcag tagacaacca 100

cggtctcagg agatgtctga tttccacaga catgcaccat atagaagaga 150

gtttccaaga aatcaaaaga gccatccaag ctaaggacac cttcccaaat 200

gtcactatcc tgtccacatt ggagactctg cagatcatta agcccttaga 250

tgtgtgctgc gtgaccaaga acctcctggc gttctacgtg gacagggtgt 300

tcaaggatca tcaggagcca aaccccaaaa tcttgagaaa aatcagcagc 350

attgccaact ctttcctcta catgcagaaa actctgcggc aatgtcagga 400

acagaggcag tgtcactgca ggcaggaagc caccaatgcc accagagtca 450

tccatgacaa ctatgatcag ctggaggtcc acgctgctgc cattaaatcc 500

ctgggagagc tcgacgtctt tctagcctgg attaataaga atcatgaagt 550

aatgttctca gcttgatgac aaggaacctg tatagtgatc cagggatgaa 600

caccccctgt gcggtttact gtgggagaca gcccaccttg aaggggaagg 650

agatggggaa ggcccccttgc agctgaaagt cccactggct ggcctcaggc 700

tgtcttattc cgcttgaaaa taggcaaaaa gtctactgtg gtatttgtaa 750

taaactctat ctgctgaaag ggcctgcagg ccatcctggg agtaaagggc 800

tgccttccca tctaatttat tgtaaagtca tatagtccat gtctgtgatg 850

tgagccaagt gatatcctgt agtacacatt gtactgagtg gtttttctga 900

ataaattcca tattttacct atga 924

<210> 84
<211> 177
<212> PRT
<213> Homo Sapien

<400> 84
Met Lys Leu Gln Cys Val Ser Leu Trp Leu Leu Gly Thr Ile Leu
1 5 10 15

Ile Leu Cys Ser Val Asp Asn His Gly Leu Arg Arg Cys Leu Ile
20 25 30

Ser Thr Asp Met His His Ile Glu Glu Ser Phe Gln Glu Ile Lys
35 40 45

Arg Ala Ile Gln Ala Lys Asp Thr Phe Pro Asn Val Thr Ile Leu
50 55 60

Ser Thr Leu Glu Thr Leu Gln Ile Ile Lys Pro Leu Asp Val Cys
65 70 75

Cys Val Thr Lys Asn Leu Leu Ala Phe Tyr Val Asp Arg Val Phe
80 85 90

Lys Asp His Gln Glu Pro Asn Pro Lys Ile Leu Arg Lys Ile Ser
95 100 105

Ser Ile Ala Asn Ser Phe Leu Tyr Met Gln Lys Thr Leu Arg Gln
110 115 120

Cys Gln Glu Gln Arg Gln Cys His Cys Arg Gln Glu Ala Thr Asn
125 130 135

Ala Thr Arg Val Ile His Asp Asn Tyr Asp Gln Leu Glu Val His
140 145 150

Ala Ala Ala Ile Lys Ser Leu Gly Glu Leu Asp Val Phe Leu Ala
155 160 165

Trp Ile Asn Lys Asn His Glu Val Met Phe Ser Ala
170 175

<210> 85
<211> 2137
<212> DNA
<213> Homo Sapien

<400> 85
gctcccagcc aagaacctcg gggccgctgc gcggtgggga ggagttcccc 50

gaaacccggc cgctaagcga ggcctcctcc tcccgcagat ccgaacggcc 100

tgggcggggt caccccggct gggacaagaa gccgccgcct gcctgcccgg 150

gcccggggag ggggctgggg ctggggccgg aggcggggtg tgagtgggtg 200

tgtgcggggg gcggaggctt gatgcaatcc cgataagaaa tgctcgggtg 250

tcttgggcac ctacccgtgg ggcccgtaag gcgctactat ataaggctgc 300

cggcccggag ccgccgcgcc gtcagagcag gagcgctgcg tccaggatct 350

agggccacga ccatcccaac ccggcactca cagccccgca gcgcatcccg 400

gtcgccgccc agcctcccgc acccccatcg ccggagctgc gccgagagcc 450

ccagggaggt gccatgcgga gcgggtgtgt ggtggtccac gtatggatcc 500

tggccggcct ctggctggcc gtggccgggc gccccctcgc cttctcggac 550
gcggggcccc acgtgcacta cggctggggc gaccccatcc gcctgcggca 600
cctgtacacc tccggccccc acgggctctc cagctgcttc ctgcgcatcc 650
gtgccgacgg cgtcgtggac tgcgcgcggg gccagagcgc gcacagtttg 700
ctggagatca aggcagtcgc tctgcggacc gtggccatca agggcgtgca 750
cagcgtgcgg tacctctgca tgggcgccga cggcaagatg caggggctgc 800
ttcagtactc ggaggaagac tgtgctttcg aggaggagat ccgcccagat 850
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cagtgccaaa cagcggcagc tgtacaagaa cagaggcttt cttccactct 950
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aggggccact tggaatctga catgttctct tcgcccctgg agaccgacag 1050
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atcataacat tgtaagcctg tagcttgccc agctgctgcc tgggccccca 1350
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cagaagacag gcagtagttt taatttcagg aacaggtgat ccactctgta 1550
aaacagcagg taaatttcac tcaaccccat gtgggaattg atctatatct 1600
ctacttccag ggaccatttg cccttcccaa atccctccag gccagaactg 1650
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attggggcct cccaggcccc ccaccttatg tcaacctgca cttcttgttc 1900
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tgctgtgtgg aagcagcggg ggaagaccta gaacccttc cccagcactt 2000

ggttttccaa catgatattt atgagtaatt tattttgata tgtacatctc 2050

ttatttttctt acattattta tgcccccaaa ttatatttat gtatgtaagt 2100

gaggtttgtt ttgtatatta aaatggagtt tgtttgt 2137

<210> 86
<211> 216
<212> PRT
<213> Homo Sapien

<400> 86

Met	Arg	Ser	Gly	Cys	Val	Val	Val	His	Val	Trp	Ile	Leu	Ala	Gly	
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Leu	Trp	Leu	Ala	Val	Ala	Gly	Arg	Pro	Leu	Ala	Phe	Ser	Asp	Ala	
				20				25						30	
Gly	Pro	His	Val	His	Tyr	Gly	Trp	Gly	Asp	Pro	Ile	Arg	Leu	Arg	
				35				40						45	
His	Leu	Tyr	Thr	Ser	Gly	Pro	His	Gly	Leu	Ser	Ser	Cys	Phe	Leu	
				50				55						60	
Arg	Ile	Arg	Ala	Asp	Gly	Val	Val	Asp	Cys	Ala	Arg	Gly	Gln	Ser	
				65				70						75	
Ala	His	Ser	Leu	Leu	Glu	Ile	Lys	Ala	Val	Ala	Leu	Arg	Thr	Val	
				80				85						90	
Ala	Ile	Lys	Gly	Val	His	Ser	Val	Arg	Tyr	Leu	Cys	Met	Gly	Ala	
				95				100						105	
Asp	Gly	Lys	Met	Gln	Gly	Leu	Leu	Gln	Tyr	Ser	Glu	Glu	Asp	Cys	
				110				115						120	
Ala	Phe	Glu	Glu	Glu	Ile	Arg	Pro	Asp	Gly	Tyr	Asn	Val	Tyr	Arg	
				125				130						135	
Ser	Glu	Lys	His	Arg	Leu	Pro	Val	Ser	Leu	Ser	Ser	Ala	Lys	Gln	
				140				145						150	
Arg	Gln	Leu	Tyr	Lys	Asn	Arg	Gly	Phe	Leu	Pro	Leu	Ser	His	Phe	
				155				160						165	
Leu	Pro	Met	Leu	Pro	Met	Val	Pro	Glu	Glu	Pro	Glu	Asp	Leu	Arg	
				170				175						180	
Gly	His	Leu	Glu	Ser	Asp	Met	Phe	Ser	Ser	Pro	Leu	Glu	Thr	Asp	
				185				190						195	
Ser	Met	Asp	Pro	Phe	Gly	Leu	Val	Thr	Gly	Leu	Glu	Ala	Val	Arg	
				200				205						210	
Ser	Pro	Ser	Phe	Glu	Lys										
				215											

<210> 87
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 87
atccgcccag atggctacaa tgtgta 26

<210> 88
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 88
gcctcccggt ctccctgagc agtgccaaac agcggcagtg ta 42

<210> 89
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 89
ccagtccggt gacaagccca aa 22

<210> 90
<211> 1857
<212> DNA
<213> Homo Sapien

<400> 90
gtctgttccc aggagtcctt cggcggctgt tgtgtcagtg gcctgatcgc 50

gatggggaca aaggcgcaag tcgagaggaa actgttgtgc ctcttcatat 100

tggcgatcct gttgtgctcc ctggcattgg gcagtgttac agtgcactct 150

tctgaacctg aagtcagaat tcctgagaat aatcctgtga agttgtcctg 200

tgcctactcg ggcttttctt ctccccgtgt ggagtggaag tttgaccaag 250

gagacaccac cagactcgtt tgctataata acaagatcac agcttcctat 300

gaggaccggg tgaccttctt gccaactggt atcaccttca agtccgtgac 350

acgggaagac actgggacat acacttgtat ggtctctgag gaaggcggca 400

acagctatgg ggaggtcaag gtcaagctca tcgtgcttgt gcctccatcc 450

aagcctacag ttaacatccc ctcctctgcc accattggga accgggcagt 500

gctgacatgc tcagaacaag atggttcccc accttctgaa tacacctggt 550

tcaaagatgg gatagtgatg cctacgaatc ccaaaagcac ccgtgccttc 600

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agtgcccgaa gtgaaggaga attcaaacag acctcgtcat tcctggtgtg 950

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ctgctgagtg gcctggaact tgtttaaagt gtttattccc catttctttg 1200

agggatcagg aaggaatcct gggtatgcca ttgacttccc ttctaagtag 1250

acagcaaaaa tggcgggggt cgcaggaatc tgcactcaac tgcccacctg 1300

gctggcaggg atctttgaat aggtatcttg agcttggttc tgggctcttt 1350

ccttgtgtac tgacgaccag ggccagctgt tctagagcgg gaattagagg 1400

ctagagcggc tgaaatggtt gtttggtgat gacactgggg tccttccatc 1450

tctggggccc actctcttct gtcttcccat gggaagtgcc actgggatcc 1500

ctctgccctg tcctcctgaa tacaagctga ctgacattga ctgtgtctgt 1550

ggaaaatggg agctcttgtt gtggagagca tagtaaattt tcagagaact 1600

tgaagccaaa aggatttaaa accgctgctc taaagaaaag aaaactggag 1650

gctgggcgca gtggctcacg cctgtaatcc cagaggctga ggcaggcgga 1700

tcacctgagg tcgggagttc gggatcagcc tgaccaacat ggagaaaccc 1750

tactggaaat acaaagttag ccaggcatgg tggtgcatgc ctgtagtccc 1800

agctgctcag gagcctggca acaagagcaa aactccagct caaaaaaaaa 1850

aaaaaaa 1857

<210> 91
<211> 299

<212> PRT
<213> Homo Sapien

<400> 91

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Met Gly Thr Lys Ala Gln Val Glu Arg Lys Leu Leu Cys Leu Phe
  1               5                  10                  15

Ile Leu Ala Ile Leu Leu Cys Ser Leu Ala Leu Gly Ser Val Thr
             20                  25                  30

Val His Ser Ser Glu Pro Glu Val Arg Ile Pro Glu Asn Asn Pro
             35                  40                  45

Val Lys Leu Ser Cys Ala Tyr Ser Gly Phe Ser Ser Pro Arg Val
             50                  55                  60

Glu Trp Lys Phe Asp Gln Gly Asp Thr Thr Arg Leu Val Cys Tyr
             65                  70                  75

Asn Asn Lys Ile Thr Ala Ser Tyr Glu Asp Arg Val Thr Phe Leu
             80                  85                  90

Pro Thr Gly Ile Thr Phe Lys Ser Val Thr Arg Glu Asp Thr Gly
             95                 100                 105

Thr Tyr Thr Cys Met Val Ser Glu Glu Gly Gly Asn Ser Tyr Gly
            110                 115                 120

Glu Val Lys Val Lys Leu Ile Val Leu Val Pro Pro Ser Lys Pro
            125                 130                 135

Thr Val Asn Ile Pro Ser Ser Ala Thr Ile Gly Asn Arg Ala Val
            140                 145                 150

Leu Thr Cys Ser Glu Gln Asp Gly Ser Pro Pro Ser Glu Tyr Thr
            155                 160                 165

Trp Phe Lys Asp Gly Ile Val Met Pro Thr Asn Pro Lys Ser Thr
            170                 175                 180

Arg Ala Phe Ser Asn Ser Ser Tyr Val Leu Asn Pro Thr Thr Gly
            185                 190                 195

Glu Leu Val Phe Asp Pro Leu Ser Ala Ser Asp Thr Gly Glu Tyr
            200                 205                 210

Ser Cys Glu Ala Arg Asn Gly Tyr Gly Thr Pro Met Thr Ser Asn
            215                 220                 225

Ala Val Arg Met Glu Ala Val Glu Arg Asn Val Gly Val Ile Val
            230                 235                 240

Ala Ala Val Leu Val Thr Leu Ile Leu Leu Gly Ile Leu Val Phe
            245                 250                 255

Gly Ile Trp Phe Ala Tyr Ser Arg Gly His Phe Asp Arg Thr Lys
            260                 265                 270
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Lys Gly Thr Ser Ser Lys Lys Val Ile Tyr Ser Gln Pro Ser Ala
                275                 280                 285

Arg Ser Glu Gly Glu Phe Lys Gln Thr Ser Ser Phe Leu Val
                290                 295
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<210> 92
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 92
tcgcggagct gtgttctgtt tccc 24

<210> 93
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 93
tgatcgcgat ggggacaaag gcgcaagctc gagaggaaac tgttgtgcct 50

<210> 94
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 94
acacctggtt caaagatggg 20

<210> 95
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 95
taggaagagt tgctgaaggc acgg 24

<210> 96
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 96
ttgccttact caggtgctac 20

<210> 97
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 97
actcagcagt ggtaggaaag 20

<210> 98
<211> 1200
<212> DNA
<213> Homo Sapien

<400> 98
cccacgcgtc cgaacctctc cagcgatggg agccgcccgc ctgctgccca 50

acctcactct gtgcttacag ctgctgattc tctgctgtca aactcagtac 100

gtgagggacc agggcgccat gaccgaccag ctgagcaggc ggcagatccg 150

cgagtaccaa ctctacagca ggaccagtgg caagcacgtg caggtcaccg 200

ggcgtcgcat ctccgccacc gccgaggacg gcaacaagtt tgccaagctc 250

atagtggaga cggacacgtt tggcagccgg gttcgcatca aaggggctga 300

gagtgagaag tacatctgta tgaacaagag gggcaagctc atcgggaagc 350

ccagcgggaa gagcaaagac tgcgtgttca cggagatcgt gctggagaac 400

aactatacgg ccttccagaa cgcccggcac gagggctggt tcatggcctt 450

cacgcggcag gggcggcccc gccaggcttc ccgcagccgc cagaaccagc 500

gcgaggccca cttcatcaag cgcctctacc aaggccagct gcccttcccc 550

aaccacgccg agaagcagaa gcagttcgag tttgtgggct ccgcccccac 600

ccgccggacc aagcgcacac ggcggcccca gcccctcacg tagtctggga 650

ggcagggggc agcagcccct gggccgcctc cccacccctt tcccttctta 700

atccaaggac tgggctgggg tggcgggagg ggagccagat ccccgaggga 750

ggaccctgag ggccgcgaag catccgagcc cccagctggg aaggggcagg 800

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aggccctgga gaggaactga gtgtcaccct gatctcaggc caccagcctc 900

tgccggcctc ccagccgggc tcctgaagcc cgctgaaagg tcagcgactg 950

aaggccttgc agacaaccgt ctggaggtgg ctgtcctcaa aatctgcttc 1000

tcggatctcc ctcagtctgc ccccagcccc caaactcctc ctggctagac 1050

tgtaggaagg gacttttgtt tgtttgtttg tttcaggaaa aaagaaaggg 1100

agagagagga aaatagaggg ttgtccactc ctcacattcc acgacccagg 1150

cctgcacccc acccccaact cccagccccg gaataaaacc attttcctgc 1200

<210> 99
<211> 205
<212> PRT
<213> Homo Sapien

<400> 99

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Leu	Leu	Ile	Leu	Cys	Cys	Gln	Thr	Gln	Tyr	Val	Arg	Asp	Gln	Gly
				20					25					30
Ala	Met	Thr	Asp	Gln	Leu	Ser	Arg	Arg	Gln	Ile	Arg	Glu	Tyr	Gln
				35					40					45
Leu	Tyr	Ser	Arg	Thr	Ser	Gly	Lys	His	Val	Gln	Val	Thr	Gly	Arg
				50					55					60
Arg	Ile	Ser	Ala	Thr	Ala	Glu	Asp	Gly	Asn	Lys	Phe	Ala	Lys	Leu
				65					70					75
Ile	Val	Glu	Thr	Asp	Thr	Phe	Gly	Ser	Arg	Val	Arg	Ile	Lys	Gly
				80					85					90
Ala	Glu	Ser	Glu	Lys	Tyr	Ile	Cys	Met	Asn	Lys	Arg	Gly	Lys	Leu
				95					100					105
Ile	Gly	Lys	Pro	Ser	Gly	Lys	Ser	Lys	Asp	Cys	Val	Phe	Thr	Glu
				110					115					120
Ile	Val	Leu	Glu	Asn	Asn	Tyr	Thr	Ala	Phe	Gln	Asn	Ala	Arg	His
				125					130					135
Glu	Gly	Trp	Phe	Met	Ala	Phe	Thr	Arg	Gln	Gly	Arg	Pro	Arg	Gln
				140					145					150
Ala	Ser	Arg	Ser	Arg	Gln	Asn	Gln	Arg	Glu	Ala	His	Phe	Ile	Lys
				155					160					165
Arg	Leu	Tyr	Gln	Gly	Gln	Leu	Pro	Phe	Pro	Asn	His	Ala	Glu	Lys
				170					175					180
Gln	Lys	Gln	Phe	Glu	Phe	Val	Gly	Ser	Ala	Pro	Thr	Arg	Arg	Thr
				185					190					195
Lys	Arg	Thr	Arg	Arg	Pro	Gln	Pro	Leu	Thr					
				200					205					

<210> 100
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 100
cagtacgtga gggaccaggg cgccatga 28

<210> 101
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 101
ccggtgacct gcacgtgctt gcca 24

<210> 102
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<220>
<221> unsure
<222> 21
<223> unknown base

<400> 102
gcggatctgc cgcctgctca nctggtcggt catggcgccc t 41

<210> 103
<211> 1679
<212> DNA
<213> Homo Sapien

<400> 103
gttgtgtcct tcagcaaaac agtggattta aatctccttg cacaagcttg 50

agagcaacac aatctatcag gaaagaaaga aagaaaaaaa ccgaacctga 100

caaaaaagaa gaaaaagaag aagaaaaaaa atcatgaaaa ccatccagcc 150

aaaaatgcac aattctatct cttgggcaat cttcacgggg ctggctgctc 200

tgtgtctctt ccaaggagtg cccgtgcgca gcggagatgc caccttcccc 250

aaagctatgg acaacgtgac ggtccggcag gggagagcg ccaccctcag 300

gtgcactatt gacaaccggg tcacccgggt ggcctggcta aaccgcagca 350

ccatcctcta tgctgggaat gacaagtggt gcctggatcc tcgcgtggtc 400

cttctgagca acacccaaac gcagtacagc atcgagatcc agaacgtgga 450

tgtgtatgac gagggccctt acacctgctc ggtgcagaca gacaaccacc 500

caaagacctc tagggtccac ctcattgtgc aagtatctcc caaaattgta 550

gagatttctt cagatatctc cattaatgaa gggaacaata ttagcctcac 600

ctgcatagca actggtagac cagagcctac ggttacttgg agacacatct 650

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catacatttc agaagccaag ggtacaggtg tccccgtggg acaaaagggg 850

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caaggatgac aaaagactga ttgaaggaaa gaaaggggtg aaagtggaaa 950

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tatgggaact acacttgcgt ggcctccaac aagctgggcc acaccaatgc 1050

cagcatcatg ctatttggtc caggcgccgt cagcgaggtg agcaacggca 1100

cgtcgaggag ggcaggctgc gtctggctgc tgcctcttct ggtcttgcac 1150

ctgcttctca aattttgatg tgagtgccac ttccccaccc gggaaaggct 1200

gccgccacca ccaccaccaa cacaacagca atggcaacac cgacagcaac 1250

caatcagata tatacaaatg aaattagaag aaacacagcc tcatgggaca 1300

gaaatttgag ggaggggaac aaagaatact ttgggggggaa aagagtttta 1350

aaaaagaaat tgaaaattgc cttgcagata tttaggtaca atggagtttt 1400

cttttcccaa acgggaagaa cacagcacac ccggcttgga cccactgcaa 1450

gctgcatcgt gcaacctctt tggtgccagt gtgggcaagg gctcagcctc 1500

tctgcccaca gagtgccccc acgtggaaca ttctggagct ggccatccca 1550

aattcaatca gtccatagag acgaacagaa tgagaccttc cggcccaagc 1600

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aaacgtgaaa taaaaagagc aaaaaaaaa 1679

<210> 104
<211> 344
<212> PRT
<213> Homo Sapien

<400> 104

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Met Lys Thr Ile Gln Pro Lys Met His Asn Ser Ile Ser Trp Ala
  1               5                  10                  15

Ile Phe Thr Gly Leu Ala Ala Leu Cys Leu Phe Gln Gly Val Pro
             20                  25                  30

Val Arg Ser Gly Asp Ala Thr Phe Pro Lys Ala Met Asp Asn Val
             35                  40                  45

Thr Val Arg Gln Gly Glu Ser Ala Thr Leu Arg Cys Thr Ile Asp
             50                  55                  60

Asn Arg Val Thr Arg Val Ala Trp Leu Asn Arg Ser Thr Ile Leu
             65                  70                  75

Tyr Ala Gly Asn Asp Lys Trp Cys Leu Asp Pro Arg Val Val Leu
             80                  85                  90

Leu Ser Asn Thr Gln Thr Gln Tyr Ser Ile Glu Ile Gln Asn Val
             95                 100                 105

Asp Val Tyr Asp Glu Gly Pro Tyr Thr Cys Ser Val Gln Thr Asp
            110                 115                 120

Asn His Pro Lys Thr Ser Arg Val His Leu Ile Val Gln Val Ser
            125                 130                 135

Pro Lys Ile Val Glu Ile Ser Ser Asp Ile Ser Ile Asn Glu Gly
            140                 145                 150

Asn Asn Ile Ser Leu Thr Cys Ile Ala Thr Gly Arg Pro Glu Pro
            155                 160                 165

Thr Val Thr Trp Arg His Ile Ser Pro Lys Ala Val Gly Phe Val
            170                 175                 180

Ser Glu Asp Glu Tyr Leu Glu Ile Gln Gly Ile Thr Arg Glu Gln
            185                 190                 195

Ser Gly Asp Tyr Glu Cys Ser Ala Ser Asn Asp Val Ala Ala Pro
            200                 205                 210

Val Val Arg Arg Val Lys Val Thr Val Asn Tyr Pro Pro Tyr Ile
            215                 220                 225

Ser Glu Ala Lys Gly Thr Gly Val Pro Val Gly Gln Lys Gly Thr
            230                 235                 240

Leu Gln Cys Glu Ala Ser Ala Val Pro Ser Ala Glu Phe Gln Trp
            245                 250                 255

Tyr Lys Asp Asp Lys Arg Leu Ile Glu Gly Lys Lys Gly Val Lys
            260                 265                 270

Val Glu Asn Arg Pro Phe Leu Ser Lys Leu Ile Phe Phe Asn Val
            275                 280                 285
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Ser Glu His Asp Tyr Gly Asn Tyr Thr Cys Val Ala Ser Asn Lys
290 295 300

Leu Gly His Thr Asn Ala Ser Ile Met Leu Phe Gly Pro Gly Ala
305 310 315

Val Ser Glu Val Ser Asn Gly Thr Ser Arg Arg Ala Gly Cys Val
320 325 330

Trp Leu Leu Pro Leu Leu Val Leu His Leu Leu Leu Lys Phe
335 340

<210> 105
<211> 1734
<212> DNA
<213> Homo Sapien

<400> 105
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gacccagagg gagggaggac agggagtcgg aaggaggagg acagaggagg 100

gcacagagac gcagagcaag ggcggcaagg aggagaccct ggtgggagga 150

agacactctg gagagagagg gggctgggca gagatgaagt tccaggggcc 200

cctggcctgc ctcctgctgg ccctctgcct gggcagtggg gaggctggcc 250

ccctgcagag cggagaggaa agcactggga caaatattgg ggaggccctt 300

ggacatggcc tgggagacgc cctgagcgaa ggggtgggaa aggccattgg 350

caaagaggcc ggaggggcag ctggctctaa agtcagtgag gcccttggcc 400

aagggaccag agaagcagtt ggcactggag tcaggcaggt tccaggcttt 450

ggcgcagcag atgctttggg caacagggtc ggggaagcag cccatgctct 500

gggaaacact gggcacgaga ttggcagaca ggcagaagat gtcattcgac 550

acggagcaga tgctgtccgc ggctcctggc aggggggtgcc tggccacagt 600

ggtgcttggg aaacttctgg aggccatggc atctttggct ctcaaggtgg 650

ccttggaggc cagggccagg gcaatcctgg aggtctgggg actccgtggg 700

tccacggata ccccggaaac tcagcaggca gctttggaat gaatcctcag 750

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caacactcag ggagctgtgg cccagcctgg ctatggttca gtgagagcca 850

gcaaccagaa tgaagggtgc acgaatcccc caccatctgg ctcaggtgga 900

ggctccagca actctggggg aggcagcggc tcacagtcgg gcagcagtgg 950

cagtggcagc aatggtgaca acaacaatgg cagcagcagt ggtggcagca 1000

gcagtggcag cagcagtggc agcagcagtg gcggcagcag tggcggcagc 1050

agtggtggca gcagtggcaa cagtggtggc agcagaggtg acagcggcag 1100

tgagtcctcc tggggatcca gcaccggctc ctcctccggc aaccacggtg 1150

ggagcggcgg aggaaatgga cataaacccg ggtgtgaaaa gccagggaat 1200

gaagcccgcg ggagcgggga atctgggatt cagggcttca gaggacaggg 1250

agtttccagc aacatgaggg aaataagcaa agagggcaat cgcctccttg 1300

gaggctctgg agacaattat cgggggcaag ggtcgagctg gggcagtgga 1350

ggaggtgacg ctgttggtgg agtcaatact gtgaactctg agacgtctcc 1400

tgggatgttt aactttgaca ctttctggaa gaattttaaa tccaagctgg 1450

gtttcatcaa ctgggatgcc ataaacaagg accagagaag ctctcgcatc 1500

ccgtgacctc cagacaagga gccaccagat tggatgggag cccccacact 1550

ccctccttaa aacaccaccc tctcatcact aatctcagcc cttgcccttg 1600

aaataaacct tagctgcccc acaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1650

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1700

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 1734

<210> 106
<211> 440
<212> PRT
<213> Homo Sapien

<400> 106

Met	Lys	Phe	Gln	Gly	Pro	Leu	Ala	Cys	Leu	Leu	Leu	Ala	Leu	Cys
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				20				25						30	
Thr	Gly	Thr	Asn	Ile	Gly	Glu	Ala	Leu	Gly	His	Gly	Leu	Gly	Asp
				35				40						45	
Ala	Leu	Ser	Glu	Gly	Val	Gly	Lys	Ala	Ile	Gly	Lys	Glu	Ala	Gly
				50				55						60	
Gly	Ala	Ala	Gly	Ser	Lys	Val	Ser	Glu	Ala	Leu	Gly	Gln	Gly	Thr
				65				70						75	
Arg	Glu	Ala	Val	Gly	Thr	Gly	Val	Arg	Gln	Val	Pro	Gly	Phe	Gly
				80				85						90	
Ala	Ala	Asp	Ala	Leu	Gly	Asn	Arg	Val	Gly	Glu	Ala	Ala	His	Ala
				95				100						105	

Leu Gly Asn Thr Gly His Glu Ile Gly Arg Gln Ala Glu Asp Val

110 115 120

Ile Arg His Gly Ala Asp Ala Val Arg Gly Ser Trp Gln Gly Val
125 130 135

Pro Gly His Ser Gly Ala Trp Glu Thr Ser Gly Gly His Gly Ile
140 145 150

Phe Gly Ser Gln Gly Gly Leu Gly Gly Gln Gly Gln Gly Asn Pro
155 160 165

Gly Gly Leu Gly Thr Pro Trp Val His Gly Tyr Pro Gly Asn Ser
170 175 180

Ala Gly Ser Phe Gly Met Asn Pro Gln Gly Ala Pro Trp Gly Gln
185 190 195

Gly Gly Asn Gly Gly Pro Pro Asn Phe Gly Thr Asn Thr Gln Gly
200 205 210

Ala Val Ala Gln Pro Gly Tyr Gly Ser Val Arg Ala Ser Asn Gln
215 220 225

Asn Glu Gly Cys Thr Asn Pro Pro Pro Ser Gly Ser Gly Gly Gly
230 235 240

Ser Ser Asn Ser Gly Gly Gly Ser Gly Ser Gln Ser Gly Ser Ser
245 250 255

Gly Ser Gly Ser Asn Gly Asp Asn Asn Asn Gly Ser Ser Ser Gly
260 265 270

Gly Ser Ser Ser Gly Ser Ser Ser Gly Ser Ser Ser Gly Gly Ser
275 280 285

Ser Gly Gly Ser Ser Gly Gly Ser Ser Gly Asn Ser Gly Gly Ser
290 295 300

Arg Gly Asp Ser Gly Ser Glu Ser Ser Trp Gly Ser Ser Thr Gly
305 310 315

Ser Ser Ser Gly Asn His Gly Gly Ser Gly Gly Gly Asn Gly His
320 325 330

Lys Pro Gly Cys Glu Lys Pro Gly Asn Glu Ala Arg Gly Ser Gly
335 340 345

Glu Ser Gly Ile Gln Gly Phe Arg Gly Gln Gly Val Ser Ser Asn
350 355 360

Met Arg Glu Ile Ser Lys Glu Gly Asn Arg Leu Leu Gly Gly Ser
365 370 375

Gly Asp Asn Tyr Arg Gly Gln Gly Ser Ser Trp Gly Ser Gly Gly
380 385 390

Gly Asp Ala Val Gly Gly Val Asn Thr Val Asn Ser Glu Thr Ser
395 400 405

Pro Gly Met Phe Asn Phe Asp Thr Phe Trp Lys Asn Phe Lys Ser
410 415 420

Lys Leu Gly Phe Ile Asn Trp Asp Ala Ile Asn Lys Asp Gln Arg
425 430 435

Ser Ser Arg Ile Pro
440

<210> 107
<211> 918
<212> DNA
<213> Homo Sapien

<400> 107
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cacacctact ttggcccctt tgacctcagg gccatgaagc tgcccagcat 200

ctcctgtcct catgagtgct ttgaggctat cctgtctctg gacaccgggt 250

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gcgggccaga cgcaatcgaa cccggacgcg ctgccgccag actactcggt 350

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acgccctccc caacctgagc caagcacccg acccgccgac gctcagcggc 450

gccgagtgct acgcctgtat cggggtccac caggatgact gcgctatcgg 500

caggtcccga cgagtccagt gtcaccagga ccagaccgcc tgcttccagg 550

gcagtggcag aatgacagtt ggcaatttct cagtccctgt gtacatcaga 600

acctgccacc ggccctcctg caccaccgag ggcaccacca gcccctggac 650

agccatcgac ctccagggct cctgctgtga ggggtacctc tgcaacagga 700

aatccatgac ccagcccttc accagtgctt cagccaccac ccctccccga 750

gcactacagg tcctggccct gctcctccca gtcctcctgc tggtggggct 800

ctcagcatag accgcccctc caggatgctg gggacagggc tcacacacct 850

cattcttgct gcttcagccc ctatcacata gctcactgga aaatgatgtt 900

aaagtaagaa ttgcaaaa 918

<210> 108
<211> 251
<212> PRT
<213> Homo Sapien

<400> 108

Met Ala Met Gly Val Pro Arg Val Ile Leu Leu Cys Leu Phe Gly
1 5 10 15

Ala Ala Leu Cys Leu Thr Gly Ser Gln Ala Leu Gln Cys Tyr Ser
20 25 30

Phe Glu His Thr Tyr Phe Gly Pro Phe Asp Leu Arg Ala Met Lys
35 40 45

Leu Pro Ser Ile Ser Cys Pro His Glu Cys Phe Glu Ala Ile Leu
50 55 60

Ser Leu Asp Thr Gly Tyr Arg Ala Pro Val Thr Leu Val Arg Lys
65 70 75

Gly Cys Trp Thr Gly Pro Pro Ala Gly Gln Thr Gln Ser Asn Pro
80 85 90

Asp Ala Leu Pro Pro Asp Tyr Ser Val Val Arg Gly Cys Thr Thr
95 100 105

Asp Lys Cys Asn Ala His Leu Met Thr His Asp Ala Leu Pro Asn
110 115 120

Leu Ser Gln Ala Pro Asp Pro Pro Thr Leu Ser Gly Ala Glu Cys
125 130 135

Tyr Ala Cys Ile Gly Val His Gln Asp Asp Cys Ala Ile Gly Arg
140 145 150

Ser Arg Arg Val Gln Cys His Gln Asp Gln Thr Ala Cys Phe Gln
155 160 165

Gly Ser Gly Arg Met Thr Val Gly Asn Phe Ser Val Pro Val Tyr
170 175 180

Ile Arg Thr Cys His Arg Pro Ser Cys Thr Thr Glu Gly Thr Thr
185 190 195

Ser Pro Trp Thr Ala Ile Asp Leu Gln Gly Ser Cys Cys Glu Gly
200 205 210

Tyr Leu Cys Asn Arg Lys Ser Met Thr Gln Pro Phe Thr Ser Ala
215 220 225

Ser Ala Thr Thr Pro Pro Arg Ala Leu Gln Val Leu Ala Leu Leu
230 235 240

Leu Pro Val Leu Leu Leu Val Gly Leu Ser Ala
245 250

<210> 109
<211> 1813
<212> DNA
<213> Homo Sapien

<400> 109

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gactccgtcc cggccaggga gggccatgat ttccctcccg gggcccctgg 150
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agtctcccag gccccttga tctgtacccc acccctatct aacaccaccc 1650

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atgaaatatg tgttgttttc atttgcaaat ttaaataaag atacataatg 1800

tttgtatgaa aaa 1813

<210> 110
<211> 390
<212> PRT
<213> Homo Sapien

<400> 110

Met	Ile	Ser	Leu	Pro	Gly	Pro	Leu	Val	Thr	Asn	Leu	Leu	Arg	Phe
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Leu	Phe	Leu	Gly	Leu	Ser	Ala	Leu	Ala	Pro	Pro	Ser	Arg	Ala	Gln
				20				25						30
Leu	Gln	Leu	His	Leu	Pro	Ala	Asn	Arg	Leu	Gln	Ala	Val	Glu	Gly
				35				40						45
Gly	Glu	Val	Val	Leu	Pro	Ala	Trp	Tyr	Thr	Leu	His	Gly	Glu	Val
				50				55						60
Ser	Ser	Ser	Gln	Pro	Trp	Glu	Val	Pro	Phe	Val	Met	Trp	Phe	Phe
				65				70						75
Lys	Gln	Lys	Glu	Lys	Glu	Asp	Gln	Val	Leu	Ser	Tyr	Ile	Asn	Gly
				80				85						90
Val	Thr	Thr	Ser	Lys	Pro	Gly	Val	Ser	Leu	Val	Tyr	Ser	Met	Pro
				95				100						105
Ser	Arg	Asn	Leu	Ser	Leu	Arg	Leu	Glu	Gly	Leu	Gln	Glu	Lys	Asp
				110				115						120
Ser	Gly	Pro	Tyr	Ser	Cys	Ser	Val	Asn	Val	Gln	Asp	Lys	Gln	Gly
				125				130						135
Lys	Ser	Arg	Gly	His	Ser	Ile	Lys	Thr	Leu	Glu	Leu	Asn	Val	Leu
				140				145						150
Val	Pro	Pro	Ala	Pro	Pro	Ser	Cys	Arg	Leu	Gln	Gly	Val	Pro	His
				155				160						165
Val	Gly	Ala	Asn	Val	Thr	Leu	Ser	Cys	Gln	Ser	Pro	Arg	Ser	Lys
				170				175						180

Pro Ala Val Gln Tyr Gln Trp Asp Arg Gln Leu Pro Ser Phe Gln
185 190 195

Thr Phe Phe Ala Pro Ala Leu Asp Val Ile Arg Gly Ser Leu Ser
200 205 210

Leu Thr Asn Leu Ser Ser Ser Met Ala Gly Val Tyr Val Cys Lys
215 220 225

Ala His Asn Glu Val Gly Thr Ala Gln Cys Asn Val Thr Leu Glu
230 235 240

Val Ser Thr Gly Pro Gly Ala Ala Val Val Ala Gly Ala Val Val
245 250 255

Gly Thr Leu Val Gly Leu Gly Leu Leu Ala Gly Leu Val Leu Leu
260 265 270

Tyr His Arg Arg Gly Lys Ala Leu Glu Glu Pro Ala Asn Asp Ile
275 280 285

Lys Glu Asp Ala Ile Ala Pro Arg Thr Leu Pro Trp Pro Lys Ser
290 295 300

Ser Asp Thr Ile Ser Lys Asn Gly Thr Leu Ser Ser Val Thr Ser
305 310 315

Ala Arg Ala Leu Arg Pro Pro His Gly Pro Pro Arg Pro Gly Ala
320 325 330

Leu Thr Pro Thr Pro Ser Leu Ser Ser Gln Ala Leu Pro Ser Pro
335 340 345

Arg Leu Pro Thr Thr Asp Gly Ala His Pro Gln Pro Ile Ser Pro
350 355 360

Ile Pro Gly Gly Val Ser Ser Ser Gly Leu Ser Arg Met Gly Ala
365 370 375

Val Pro Val Met Val Pro Ala Gln Ser Gln Ala Gly Ser Leu Val
380 385 390

<210> 111
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 111
agggtctcca ggagaaagac tc 22

<210> 112
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 112
attgtgggcc ttgcagacat agac 24

<210> 113
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 113
ggccacagca tcaaaacctt agaactcaat gtactggttc ctccagctcc 50

<210> 114
<211> 2479
<212> DNA
<213> Homo Sapien

<400> 114
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ttgcacatgg aggacagcag caaagagggc aacacaggct gataagacca 100

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gctggagttc tggacttcaa cagaacccca tccagtcatt ttgattttgc 200

tgtttatttt ttttttcttt ttctttttcc caccacattg tattttattt 250

ccgtacttca gaaatgggcc tacagaccac aaagtggccc agccatgggg 300

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gtgtccaaac tcctggcctg ccctagtgtg tgccgctgcg acaggaactt 400

tgtctactgt aatgagcgaa gcttgacctc agtgcctctt gggatcccgg 450

agggcgtaac cgtactctac ctccacaaca accaaattaa taatgctgga 500

tttcctgcag aactgcacaa tgtacagtcg gtgcacacgg tctacctgta 550

tggcaaccaa ctggacgaat tccccatgaa ccttcccaag aatgtcagag 600

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gcccagctct tgaagcttga agagctgcac ctggatgaca actccatatc 700

cacagtgggg gtggaagacg gggccttccg ggaggctatt agcctcaaat 750

tgttgttttt gtctaagaat cacctgagca gtgtgcctgt tgggcttcct 800

gtggacttgc aagagctgag agtggatgaa aatcgaattg ctgtcatatc 850

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ggaacctcct gaccaacaag ggtatcgccg agggcacctt cagccatctc 950

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caactccatc ctggagatga cagaaaccag ttttcagatc gtctccttaa 2100

ataacgatca actccttaaa ggagatttca gactgcagcc catttacacc 2150

ccaaatgggg gcattaatta cacagactgc catatcccca acaacatgcg 2200

atactgcaac agcagcgtgc cagacctgga gcactgccat acgtgacagc 2250

cagaggccca gcgttatcaa ggcggacaat tagactcttg agaacacact 2300

cgtgtgtgca cataaagaca cgcagattac atttgataaa tgttacacag 2350

atgcatttgt gcatttgaat actctgtaat ttatacggtg tactatataa 2400

tgggatttaa aaaaagtgct atcttttcta tttcaagtta attacaaaca 2450

gttttgtaac tctttgcttt ttaaatctt 2479

<210> 115
<211> 660
<212> PRT
<213> Homo Sapien

<400> 115
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Leu Lys Ser Trp Leu Ile Ile Ser Leu Gly Leu Tyr Ser Gln Val
20 25 30

Ser Lys Leu Leu Ala Cys Pro Ser Val Cys Arg Cys Asp Arg Asn
35 40 45

Phe Val Tyr Cys Asn Glu Arg Ser Leu Thr Ser Val Pro Leu Gly
50 55 60

Ile Pro Glu Gly Val Thr Val Leu Tyr Leu His Asn Asn Gln Ile
65 70 75

Asn Asn Ala Gly Phe Pro Ala Glu Leu His Asn Val Gln Ser Val
80 85 90

His Thr Val Tyr Leu Tyr Gly Asn Gln Leu Asp Glu Phe Pro Met
95 100 105

Asn Leu Pro Lys Asn Val Arg Val Leu His Leu Gln Glu Asn Asn
110 115 120

Ile Gln Thr Ile Ser Arg Ala Ala Leu Ala Gln Leu Leu Lys Leu
125 130 135

Glu Glu Leu His Leu Asp Asp Asn Ser Ile Ser Thr Val Gly Val
140 145 150

Glu Asp Gly Ala Phe Arg Glu Ala Ile Ser Leu Lys Leu Leu Phe
155 160 165

Leu Ser Lys Asn His Leu Ser Ser Val Pro Val Gly Leu Pro Val
170 175 180

Asp Leu Gln Glu Leu Arg Val Asp Glu Asn Arg Ile Ala Val Ile
185 190 195

Ser Asp Met Ala Phe Gln Asn Leu Thr Ser Leu Glu Arg Leu Ile
200 205 210

Val Asp Gly Asn Leu Leu Thr Asn Lys Gly Ile Ala Glu Gly Thr
215 220 225

Phe Ser His Leu Thr Lys Leu Lys Glu Phe Ser Ile Val Arg Asn

230 235 240

Ser Leu Ser His Pro Pro Pro Asp Leu Pro Gly Thr His Leu Ile
245 250 255

Arg Leu Tyr Leu Gln Asp Asn Gln Ile Asn His Ile Pro Leu Thr
260 265 270

Ala Phe Ser Asn Leu Arg Lys Leu Glu Arg Leu Asp Ile Ser Asn
275 280 285

Asn Gln Leu Arg Met Leu Thr Gln Gly Val Phe Asp Asn Leu Ser
290 295 300

Asn Leu Lys Gln Leu Thr Ala Arg Asn Asn Pro Trp Phe Cys Asp
305 310 315

Cys Ser Ile Lys Trp Val Thr Glu Trp Leu Lys Tyr Ile Pro Ser
320 325 330

Ser Leu Asn Val Arg Gly Phe Met Cys Gln Gly Pro Glu Gln Val
335 340 345

Arg Gly Met Ala Val Arg Glu Leu Asn Met Asn Leu Leu Ser Cys
350 355 360

Pro Thr Thr Thr Pro Gly Leu Pro Leu Phe Thr Pro Ala Pro Ser
365 370 375

Thr Ala Ser Pro Thr Thr Gln Pro Pro Thr Leu Ser Ile Pro Asn
380 385 390

Pro Ser Arg Ser Tyr Thr Pro Pro Thr Pro Thr Thr Ser Lys Leu
395 400 405

Pro Thr Ile Pro Asp Trp Asp Gly Arg Glu Arg Val Thr Pro Pro
410 415 420

Ile Ser Glu Arg Ile Gln Leu Ser Ile His Phe Val Asn Asp Thr
425 430 435

Ser Ile Gln Val Ser Trp Leu Ser Leu Phe Thr Val Met Ala Tyr
440 445 450

Lys Leu Thr Trp Val Lys Met Gly His Ser Leu Val Gly Gly Ile
455 460 465

Val Gln Glu Arg Ile Val Ser Gly Glu Lys Gln His Leu Ser Leu
470 475 480

Val Asn Leu Glu Pro Arg Ser Thr Tyr Arg Ile Cys Leu Val Pro
485 490 495

Leu Asp Ala Phe Asn Tyr Arg Ala Val Glu Asp Thr Ile Cys Ser
500 505 510

Glu Ala Thr Thr His Ala Ser Tyr Leu Asn Asn Gly Ser Asn Thr
515 520 525

Ala Ser Ser His Glu Gln Thr Thr Ser His Ser Met Gly Ser Pro
530 535 540

Phe Leu Leu Ala Gly Leu Ile Gly Gly Ala Val Ile Phe Val Leu
545 550 555

Val Val Leu Leu Ser Val Phe Cys Trp His Met His Lys Lys Gly
560 565 570

Arg Tyr Thr Ser Gln Lys Trp Lys Tyr Asn Arg Gly Arg Arg Lys
575 580 585

Asp Asp Tyr Cys Glu Ala Gly Thr Lys Lys Asp Asn Ser Ile Leu
590 595 600

Glu Met Thr Glu Thr Ser Phe Gln Ile Val Ser Leu Asn Asn Asp
605 610 615

Gln Leu Leu Lys Gly Asp Phe Arg Leu Gln Pro Ile Tyr Thr Pro
620 625 630

Asn Gly Gly Ile Asn Tyr Thr Asp Cys His Ile Pro Asn Asn Met
635 640 645

Arg Tyr Cys Asn Ser Ser Val Pro Asp Leu Glu His Cys His Thr
650 655 660

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<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 116
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<210> 117
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 117
gcaggacaac cagataaacc ac 22

<210> 118
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 118

acgcagattt gagaaggctg tc 22

<210> 119
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 119
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<210> 120
<211> 2857
<212> DNA
<213> Homo Sapien

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actgctgcgt tttatgttgg gaattcctct cctatggcct tgtcttggag 100

caacagaaaa ctctcaaaca aagaaagtca agcagccagt gcgatctcat 150

ttgagagtga agcgtggctg ggtgtggaac caatttttg taccagagga 200

aatgaatacg actagtcatc acatcggcca gctaagatct gatttagaca 250

atggaaacaa ttctttccag tacaagcttt tgggagctgg agctggaagt 300

acttttatca ttgatgaaag aacaggtgac atatatgcca tacagaagct 350

tgatagagag gagcgatccc tctacatctt aagagcccag gtaatagaca 400

tcgctactgg aagggctgtg gaacctgagt ctgagtttgt catcaaagtt 450

tcggatatca atgacaatga accaaaattc ctagatgaac cttatgaggc 500

cattgtacca gagatgtctc cagaaggaac attagttatc caggtgacag 550

caagtgatgc tgacgatccc tcaagtggta ataatgctcg tctcctctac 600

agcttacttc aaggccagcc atatttttct gttgaaccaa caacaggagt 650

cataagaata tcttctaaaa tggatagaga actgcaagat gagtattggg 700

taatcattca agccaaggac atgattggtc agccaggagc gttgtctgga 750

acaacaagtg tattaattaa actttcagat gttaatgaca ataagcctat 800

atttaaagaa agtttatacc gcttgactgt ctctgaatct gcacccactg 850

ggacttctat aggaacaatc atggcatatg ataatgacat aggagagaat 900

gcagaaatgg attacagcat tgaagaggat gattcgcaaa catttgacat 950

tattactaat catgaaactc aagaaggaat agttatatta aaaaagaaag 1000

tggattttga gcaccagaac cactacggta ttagagcaaa agttaaaaac 1050

catcatgttc ctgagcagct catgaagtac cacactgagg cttccaccac 1100

tttcattaag atccaggtgg aagatgttga tgagcctcct cttttcctcc 1150

ttccatatta tgtatttgaa gtttttgaag aaaccccaca gggatcattt 1200

gtaggcgtgg tgtctgccac agacccagac aataggaaat ctcctatcag 1250

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tcactacaag taactcactg gatcgtgaaa tcagtgcttg gtacaaccta 1350

agtattacag ccacagaaaa atacaatata gaacagatct cttcgatccc 1400

actgtatgtg caagttctta acatcaatga tcatgctcct gagttctctc 1450

aatactatga gacttatgtt tgtgaaaatg caggctctgg tcaggtaatt 1500

cagactatca gtgcagtgga tagagatgaa tccatagaag agcaccattt 1550

ttactttaat ctatctgtag aagacactaa caattcaagt tttacaatca 1600

tagataatca agataacaca gctgtcattt tgactaatag aactggtttt 1650

aaccttcaag aagaacctgt cttctacatc tccatcttaa ttgccgacaa 1700

tggaatcccg tcacttacaa gtacaaacac ccttaccatc catgtctgtg 1750

actgtggtga cagtgggagc acacagacct gccagtacca ggagcttgtg 1800

ctttccatgg gattcaagac agaagttatc attgctattc tcatttgcat 1850

tatgatcata tttgggttta tttttttgac tttgggttta aaacaacgga 1900

gaaaacagat tctatttcct gagaaaagtg aagatttcag agagaatata 1950

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tatagcagag ctgaggagta gtaccataat gcgggaacgc aagactcgga 2050

aaaccacaag cgctgagatc aggagcctat acaggcagtc tttgcaagtt 2100

ggccccgaca gtgccatatt caggaaattc attctggaaa agctcgaaga 2150

agctaatact gatccgtgtg cccctccttt tgattccctc cagacctacg 2200

cttttgaggg aacagggtca ttagctggat ccctgagctc cttagaatca 2250

gcagtctctg atcaggatga aagctatgat taccttaatg agttgggacc 2300

tcgctttaaa agattagcat gcatgtttgg ttctgcagtg cagtcaaata 2350

attagggctt tttaccatca aaatttttaa aagtgctaat gtgtattcga 2400

acccaatggt agtcttaaag agttttgtgc cctggctcta tggcggggaa 2450

agccctagtc tatggagttt tctgatttcc ctggagtaaa tactccatgg 2500

ttattttaag ctacctacat gctgtcattg aacagagatg tggggagaaa 2550

tgtaaacaat cagctcacag gcatcaatac aaccagattt gaagtaaaat 2600

aatgtaggaa gatattaaaa gtagatgaga ggacacaaga tgtagtcgat 2650

ccttatgcga ttatatcatt atttacttag gaaagagtaa aaataccaaa 2700

cgagaaaatt taaaggagca aaaatttgca agtcaaatag aaatgtacaa 2750

atcgagataa catttacatt tctatcatat tgacatgaaa attgaaaatg 2800

tatagtcaga gaaattttca tgaattattc catgaagtat tgtttccttt 2850

atttaaa 2857

<210> 121
<211> 772
<212> PRT
<213> Homo Sapien

<400> 121

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				20					25					30	
Val	Lys	Gln	Pro	Val	Arg	Ser	His	Leu	Arg	Val	Lys	Arg	Gly	Trp	
				35					40					45	
Val	Trp	Asn	Gln	Phe	Phe	Val	Pro	Glu	Glu	Met	Asn	Thr	Thr	Ser	
				50					55					60	
His	His	Ile	Gly	Gln	Leu	Arg	Ser	Asp	Leu	Asp	Asn	Gly	Asn	Asn	
				65					70					75	
Ser	Phe	Gln	Tyr	Lys	Leu	Leu	Gly	Ala	Gly	Ala	Gly	Ser	Thr	Phe	
				80					85					90	
Ile	Ile	Asp	Glu	Arg	Thr	Gly	Asp	Ile	Tyr	Ala	Ile	Gln	Lys	Leu	
				95					100					105	
Asp	Arg	Glu	Glu	Arg	Ser	Leu	Tyr	Ile	Leu	Arg	Ala	Gln	Val	Ile	
				110					115					120	
Asp	Ile	Ala	Thr	Gly	Arg	Ala	Val	Glu	Pro	Glu	Ser	Glu	Phe	Val	
				125					130					135	
Ile	Lys	Val	Ser	Asp	Ile	Asn	Asp	Asn	Glu	Pro	Lys	Phe	Leu	Asp	
				140					145					150	
Glu	Pro	Tyr	Glu	Ala	Ile	Val	Pro	Glu	Met	Ser	Pro	Glu	Gly	Thr	
				155					160					165	
Leu	Val	Ile	Gln	Val	Thr	Ala	Ser	Asp	Ala	Asp	Asp	Pro	Ser	Ser	

170 175 180

Gly Asn Asn Ala Arg Leu Leu Tyr Ser Leu Leu Gln Gly Gln Pro
185 190 195

Tyr Phe Ser Val Glu Pro Thr Thr Gly Val Ile Arg Ile Ser Ser
200 205 210

Lys Met Asp Arg Glu Leu Gln Asp Glu Tyr Trp Val Ile Ile Gln
215 220 225

Ala Lys Asp Met Ile Gly Gln Pro Gly Ala Leu Ser Gly Thr Thr
230 235 240

Ser Val Leu Ile Lys Leu Ser Asp Val Asn Asp Asn Lys Pro Ile
245 250 255

Phe Lys Glu Ser Leu Tyr Arg Leu Thr Val Ser Glu Ser Ala Pro
260 265 270

Thr Gly Thr Ser Ile Gly Thr Ile Met Ala Tyr Asp Asn Asp Ile
275 280 285

Gly Glu Asn Ala Glu Met Asp Tyr Ser Ile Glu Glu Asp Asp Ser
290 295 300

Gln Thr Phe Asp Ile Ile Thr Asn His Glu Thr Gln Glu Gly Ile
305 310 315

Val Ile Leu Lys Lys Lys Val Asp Phe Glu His Gln Asn His Tyr
320 325 330

Gly Ile Arg Ala Lys Val Lys Asn His His Val Pro Glu Gln Leu
335 340 345

Met Lys Tyr His Thr Glu Ala Ser Thr Thr Phe Ile Lys Ile Gln
350 355 360

Val Glu Asp Val Asp Glu Pro Pro Leu Phe Leu Leu Pro Tyr Tyr
365 370 375

Val Phe Glu Val Phe Glu Glu Thr Pro Gln Gly Ser Phe Val Gly
380 385 390

Val Val Ser Ala Thr Asp Pro Asp Asn Arg Lys Ser Pro Ile Arg
395 400 405

Tyr Ser Ile Thr Arg Ser Lys Val Phe Asn Ile Asn Asp Asn Gly
410 415 420

Thr Ile Thr Thr Ser Asn Ser Leu Asp Arg Glu Ile Ser Ala Trp
425 430 435

Tyr Asn Leu Ser Ile Thr Ala Thr Glu Lys Tyr Asn Ile Glu Gln
440 445 450

Ile Ser Ser Ile Pro Leu Tyr Val Gln Val Leu Asn Ile Asn Asp
455 460 465

His Ala Pro Glu Phe Ser Gln Tyr Tyr Glu Thr Tyr Val Cys Glu
470 475 480

Asn Ala Gly Ser Gly Gln Val Ile Gln Thr Ile Ser Ala Val Asp
485 490 495

Arg Asp Glu Ser Ile Glu Glu His His Phe Tyr Phe Asn Leu Ser
500 505 510

Val Glu Asp Thr Asn Asn Ser Ser Phe Thr Ile Ile Asp Asn Gln
515 520 525

Asp Asn Thr Ala Val Ile Leu Thr Asn Arg Thr Gly Phe Asn Leu
530 535 540

Gln Glu Glu Pro Val Phe Tyr Ile Ser Ile Leu Ile Ala Asp Asn
545 550 555

Gly Ile Pro Ser Leu Thr Ser Thr Asn Thr Leu Thr Ile His Val
560 565 570

Cys Asp Cys Gly Asp Ser Gly Ser Thr Gln Thr Cys Gln Tyr Gln
575 580 585

Glu Leu Val Leu Ser Met Gly Phe Lys Thr Glu Val Ile Ile Ala
590 595 600

Ile Leu Ile Cys Ile Met Ile Ile Phe Gly Phe Ile Phe Leu Thr
605 610 615

Leu Gly Leu Lys Gln Arg Arg Lys Gln Ile Leu Phe Pro Glu Lys
620 625 630

Ser Glu Asp Phe Arg Glu Asn Ile Phe Gln Tyr Asp Asp Glu Gly
635 640 645

Gly Gly Glu Glu Asp Thr Glu Ala Phe Asp Ile Ala Glu Leu Arg
650 655 660

Ser Ser Thr Ile Met Arg Glu Arg Lys Thr Arg Lys Thr Thr Ser
665 670 675

Ala Glu Ile Arg Ser Leu Tyr Arg Gln Ser Leu Gln Val Gly Pro
680 685 690

Asp Ser Ala Ile Phe Arg Lys Phe Ile Leu Glu Lys Leu Glu Glu
695 700 705

Ala Asn Thr Asp Pro Cys Ala Pro Pro Phe Asp Ser Leu Gln Thr
710 715 720

Tyr Ala Phe Glu Gly Thr Gly Ser Leu Ala Gly Ser Leu Ser Ser
725 730 735

Leu Glu Ser Ala Val Ser Asp Gln Asp Glu Ser Tyr Asp Tyr Leu
740 745 750

Asn Glu Leu Gly Pro Arg Phe Lys Arg Leu Ala Cys Met Phe Gly

10065211.062102

755 760 765

Ser Ala Val Gln Ser Asn Asn
770

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<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 122
cttgactgtc tctgaatctg caccc 25

<210> 123
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 123
aagtggtgga agcctccagt gtgg 24

<210> 124
<211> 52
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 124
ccactacggt attagagcaa aagttaaaaa ccatcatggt tcctggagca 50

gc 52

<210> 125
<211> 1152
<212> DNA
<213> Homo Sapien

<400> 125
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gtctgcaatg gccgccctgc agaaatctgt gagctctttc cttatgggga 100

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gcagctgcgc ccatcagctc ccactgcagg cttgacaagt ccaacttcca 200

gcagccctat atcaccaacc gcaccttcat gctggctaag gaggctagct 250

tggctgataa caacacagac gttcgtctca ttggggagaa actgttccac 300

ggagtcagta tgagtgagcg ctgctatctg atgaagcagg tgctgaactt 350

cacccttgaa gaagtgctgt tccctcaatc tgataggttc cagccttata 400

tgcaggaggt ggtgcccttc ctggccaggc tcagcaacag gctaagcaca 450

tgtcatattg aaggtgatga cctgcatatc cagaggaatg tgcaaaagct 500

gaaggacaca gtgaaaaagc ttggagagag tggagagatc aaagcaattg 550

gagaactgga tttgctgttt atgtctctga gaaatgcctg catttgacca 600

gagcaaagct gaaaaatgaa taactaaccc cctttccctg ctagaaataa 650

caattagatg ccccaaagcg attttttta accaaaagga agatgggaag 700

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tactttccat tcctttaggg gaaaaaaccc ctaaatagct tcatgtttcc 950

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cc 1152

<210> 126
<211> 179
<212> PRT
<213> Homo Sapien

<400> 126
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Leu Ala Thr Ser Cys Leu Leu Leu Leu Ala Leu Leu Val Gln Gly
20 25 30

Gly Ala Ala Ala Pro Ile Ser Ser His Cys Arg Leu Asp Lys Ser
35 40 45

Asn Phe Gln Gln Pro Tyr Ile Thr Asn Arg Thr Phe Met Leu Ala
50 55 60

Lys Glu Ala Ser Leu Ala Asp Asn Asn Thr Asp Val Arg Leu Ile
65 70 75

Gly Glu Lys Leu Phe His Gly Val Ser Met Ser Glu Arg Cys Tyr

80 85 90

Leu Met Lys Gln Val Leu Asn Phe Thr Leu Glu Glu Val Leu Phe
95 100 105

Pro Gln Ser Asp Arg Phe Gln Pro Tyr Met Gln Glu Val Val Pro
110 115 120

Phe Leu Ala Arg Leu Ser Asn Arg Leu Ser Thr Cys His Ile Glu
125 130 135

Gly Asp Asp Leu His Ile Gln Arg Asn Val Gln Lys Leu Lys Asp
140 145 150

Thr Val Lys Lys Leu Gly Glu Ser Gly Glu Ile Lys Ala Ile Gly
155 160 165

Glu Leu Asp Leu Leu Phe Met Ser Leu Arg Asn Ala Cys Ile
170 175

<210> 127
<211> 2557
<212> DNA
<213> Homo Sapien

<400> 127
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gccggggcca tccctagaca gaggaaagtt cctgcagagc cgaccagccc 200

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caagtggcct ctcctccccg cggttgttgt tcagtgtcgg gtgagggctg 400

cgagtgtggc aagttgcaaa gagagcctca gaggtccgaa gagcgctgcg 450

ctcctactcg cgttcgcttc ttcctcttct cggttcccta ctgtgaaatc 500

gcagcgacat ttacaaaggc ctccgggtcc taccgagacc gatccgcagc 550

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ggacagtgga tgccctgaag agtcaaaaga gaagatgtgt gagaatacag 1750
aaccagtgga aacttcttct cgaaccacca caaccgtagg agcgacaacc 1800
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aagtttagaa gaggctctgg acatcctgcc tatgctgaag ttgaaccagt 2150
tggagagaaa gaaggcttta ttgtatcaga gcagtgctaa aatttctagg 2200
acagaacaac accagtactg gtttacaggt gttaagacta aaattttgcc 2250

tataccttta agacaaacaa acaaacacac acacaaacaa gctctaagct 2300

gctgtagcct gaagaagaca agatttctgg acaagctcag cccaggaaac 2350

aaagggtaaa caaaaaacta aaacttatac aagataccat ttacactgaa 2400

catagaattc cctagtggaa tgtcatctat agttcactcg gaacatctcc 2450

cgtggactta tctgaagtat gacaagatta taatgctttt ggcttaggtg 2500

cagggttgca aagggatcag aaaaaaaaaa tcataataaa gctttagttc 2550

atgaggg 2557

<210> 128
<211> 529
<212> PRT
<213> Homo Sapien

<400> 128
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Leu Leu Cys His Phe Phe Thr Asp Gln Phe Gln Phe Ala Asp Gly
20 25 30

Lys Pro Gly Asp Gln Ile Leu Asp Trp Gln Tyr Gly Val Thr Gln
35 40 45

Ala Phe Pro His Thr Glu Glu Glu Val Glu Val Asp Ser His Ala
50 55 60

Tyr Ser His Arg Trp Lys Arg Asn Leu Asp Phe Leu Lys Ala Val
65 70 75

Asp Thr Asn Arg Ala Ser Val Gly Gln Asp Ser Pro Glu Pro Arg
80 85 90

Ser Phe Thr Asp Leu Leu Leu Asp Asp Gly Gln Asp Asn Asn Thr
95 100 105

Gln Ile Glu Glu Asp Thr Asp His Asn Tyr Tyr Ile Ser Arg Ile
110 115 120

Tyr Gly Pro Ser Asp Ser Ala Ser Arg Asp Leu Trp Val Asn Ile
125 130 135

Asp Gln Met Glu Lys Asp Lys Val Lys Ile His Gly Ile Leu Ser
140 145 150

Asn Thr His Arg Gln Ala Ala Arg Val Asn Leu Ser Phe Asp Phe
155 160 165

Pro Phe Tyr Gly His Phe Leu Arg Glu Ile Thr Val Ala Thr Gly
170 175 180

Gly Phe Ile Tyr Thr Gly Glu Val Val His Arg Met Leu Thr Ala
185 190 195

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Thr Gln Tyr Ile Ala Pro Leu Met Ala Asn Phe Asp Pro Ser Val
                200                 205                 210

Ser Arg Asn Ser Thr Val Arg Tyr Phe Asp Asn Gly Thr Ala Leu
                215                 220                 225

Val Val Gln Trp Asp His Val His Leu Gln Asp Asn Tyr Asn Leu
                230                 235                 240

Gly Ser Phe Thr Phe Gln Ala Thr Leu Leu Met Asp Gly Arg Ile
                245                 250                 255

Ile Phe Gly Tyr Lys Glu Ile Pro Val Leu Val Thr Gln Ile Ser
                260                 265                 270

Ser Thr Asn His Pro Val Lys Val Gly Leu Ser Asp Ala Phe Val
                275                 280                 285

Val Val His Arg Ile Gln Gln Ile Pro Asn Val Arg Arg Arg Thr
                290                 295                 300

Ile Tyr Glu Tyr His Arg Val Glu Leu Gln Met Ser Lys Ile Thr
                305                 310                 315

Asn Ile Ser Ala Val Glu Met Thr Pro Leu Pro Thr Cys Leu Gln
                320                 325                 330

Phe Asn Arg Cys Gly Pro Cys Val Ser Ser Gln Ile Gly Phe Asn
                335                 340                 345

Cys Ser Trp Cys Ser Lys Leu Gln Arg Cys Ser Ser Gly Phe Asp
                350                 355                 360

Arg His Arg Gln Asp Trp Val Asp Ser Gly Cys Pro Glu Glu Ser
                365                 370                 375

Lys Glu Lys Met Cys Glu Asn Thr Glu Pro Val Glu Thr Ser Ser
                380                 385                 390

Arg Thr Thr Thr Thr Val Gly Ala Thr Thr Thr Gln Phe Arg Val
                395                 400                 405

Leu Thr Thr Thr Arg Arg Ala Val Thr Ser Gln Phe Pro Thr Ser
                410                 415                 420

Leu Pro Thr Glu Asp Asp Thr Lys Ile Ala Leu His Leu Lys Asp
                425                 430                 435

Asn Gly Ala Ser Thr Asp Asp Ser Ala Ala Glu Lys Lys Gly Gly
                440                 445                 450

Thr Leu His Ala Gly Leu Ile Ile Gly Ile Leu Ile Leu Val Leu
                455                 460                 465

Ile Val Ala Thr Ala Ile Leu Val Thr Val Tyr Met Tyr His His
                470                 475                 480

Pro Thr Ser Ala Ala Ser Ile Phe Phe Ile Glu Arg Arg Pro Ser
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485 490 495

Arg Trp Pro Ala Met Lys Phe Arg Arg Gly Ser Gly His Pro Ala
500 505 510

Tyr Ala Glu Val Glu Pro Val Gly Glu Lys Glu Gly Phe Ile Val
515 520 525

Ser Glu Gln Cys

<210> 129
<211> 4834
<212> DNA
<213> Homo Sapien

<220>
<221> unsure
<222> 3784
<223> unknown base

<400> 129
gcagccctag cagggatgga catgatgctg ttggtgcagg gtgcttgttg 50

ctcgaaccag tggctggcgg cggtgctcct cagcctgtgc tgcctgctac 100

cctcctgcct cccggctgga cagagtgtgg acttcccctg ggcggccgtg 150

gacaacatga tggtcagaaa aggggacacg gcggtgctta ggtgttattt 200

ggaagatgga gcttcaaagg gtgcctggct gaaccggtca agtattattt 250

ttgcgggagg tgataagtgg tcagtggatc ctcgagtttc aatttcaaca 300

ttgaataaaa gggactacag cctccagata cagaatgtag atgtgacaga 350

tgatggccca tacacgtgtt ctgttcagac tcaacataca cccagaacaa 400

tgcaggtgca tctaactgtg caagttcctc ctaagatata tgacatctca 450

aatgatatga ccgtcaatga aggaaccaac gtcactctta cttgtttggc 500

cactgggaaa ccagagcctt ccatttcttg gcgacacatc tccccatcag 550

caaaaccatt tgaaaatgga caatatttgg acatttatgg aattacaagg 600

gaccaggctg gggaatatga atgcagtgcg gaaaatgatg tgtcattccc 650

agatgtgagg aaagtaaaag ttgttgtcaa ctttgctcct actattcagg 700

aaattaaatc tggcaccgtg acccccggac gcagtggcct gataagatgt 750

gaaggtgcag gtgtgccgcc tccagccttt gaatggtaca aaggagagaa 800

gaagctcttc aatggccaac aaggaattat tattcaaaat tttagcacaa 850

gatccattct cactgttacc aacgtgacac aggagcactt cggcaattat 900

acttgtgtgg ctgccaacaa gctaggcaca accaatgcga gcctgcctct 950

taaccctcca agtacagccc agtatggaat taccgggagc gctgatgttc 1000

ttttctcctg ctggtacctt gtgttgacac tgtcctcttt caccagcata 1050

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tgtttgtaat ctacaacttt tcaaaagcat tcagtcatgg tctgctaggt 1400

tgcaggctgt agtttacaaa aacgaatatt gcagtgaata tgtgattctt 1450

taaggctgca atacaagcat tcagttccct gtttcaataa gagtcaatcc 1500

acatttacaa agatgcattt ttttcttttt tgataaaaaa gcaaataata 1550

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caataatatt tttctctttg tctccaacta atataaaatg ttttgctaaa 1750

tcttacaatt tgaaagtaaa aataaaccag agtgatcaag ttaaaccata 1800

cactatctct aagtaacgaa ggagctattg gactgtaaaa atctcttcct 1850

gcactgacaa tggggtttga gaattttgcc ccacactaac tcagttcttg 1900

tgatgagaga caatttaata acagtatagt aaatatacca tatgatttct 1950

ttagttgtag ctaaatgtta gatccaccgt gggaaatcat tccctttaaa 2000

atgacagcac agtccactca aaggattgcc tagcaataca gcatcttttc 2050

ctttcactag tccaagccaa aaattttaag atgatttgtc agaaagggca 2100

caaagtccta tcacctaata ttacaagagt tggtaagcgc tcatcattaa 2150

ttttattttg tggcagctaa gttagtatga cagaggcagt gctcctgtgg 2200

acaggagcat tttgcatatt ttccatctga aagtatcact cagttgatag 2250

tctggaatgc atgttatata ttttaaaact tccaaaatat attataacaa 2300

acattctata tcggtatgta gcagaccaat ctctaaaata gctaattctt 2350

caataaaatc tttctatata gccatttcag tgcaaacaag taaaatcaaa 2400
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aattattgtg aatgttaaat tatttctact ataaagaagc aaaactacat 2550
ttttgaagga aaatgctgtt actctaacat taatttacag gaatagtttg 2600
atggtttcac tctttactaa agaaaggcca tcaccttgaa agccatttta 2650
caggtttgat gaagttacca atttcagtac acctaaattt ctacaaatag 2700
tccccttta caagttgtaa caacaaagac cctataataa aattagatac 2750
aagaaatttt gcagtggtta tacatatttg agatatctag tatgttgccc 2800
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cttactagaa atagtggtgc taccacaaaa aatgttaacc atcagtacca 3200
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tcacagcagc attcctagtc cttaggccct cggacagagt gaaatcatga 3550
gtatttatga gttcaatatt gtcaaataag gctacagtat ttgctttttt 3600
gtgtgaatgt attgcatata atgttcaagt agatgatttt acatttatgg 3650
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tccacttgtg ggactccttt tgttgcccct attttttttt aaagaaggaa 3850

gaaagaaaaa taagtagcag tttaaaaatg agaatggaga gaaaagaaaa 3900

agaatgaaaa ggaaaggcag taaagaggga aaaaaaagga aggatggaag 3950

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tgagagggaa ggaagaatca gagtattagg gtagttaact tacacatttg 4050

cattcttagt ttaactgcaa gtggtgtaac tatgtttttc aatgatcgca 4100

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atataataaa aagtactgcc caagttatag taatgtgggt gtttttgaga 4200

cactaaaaga tttgagaggg agaatttcaa acttaaagcc acttttgggg 4250

ggtttataac ttaactgaaa aattaatgct tcatcataac atttaagcta 4300

tatctagaaa gtagactgga gaactgagaa aattacccag gtaattcagg 4350

gaaaaaaaaa aatatatata tatataaata cccctacatt tgaagtcaga 4400

aaactctgaa aaactgaatt atcaaagtca atcatctata atgatcaaat 4450

ttactgaaca attgttaatt tatccattgt gcttagcttt gtgacacagc 4500

caaaagttac ctatttaatc ttttcaataa aaattgtttt ttgaaatcca 4550

gaaatgattt aaaaagaggt caggttttta actatttatt gaagtatgtg 4600

gatgtacagt atttcaatag atatgaatat gaataaatgg tatgccttaa 4650

gattctttga atatgtattt actttaaaga ctggaaaaag ctcttcctgt 4700

cttttagtaa aacatccata tttcataacc tgatgtaaaa tatgttgtac 4750

tgtttccaat aggtgaatat aaactcagtt tatcaattaa aaaaaaaaaa 4800

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 4834

<210> 130
<211> 354
<212> PRT
<213> Homo Sapien

<400> 130

Met Asp Met Met Leu Leu Val Gln Gly Ala Cys Cys Ser Asn Gln
1 5 10 15

Trp Leu Ala Ala Val Leu Leu Ser Leu Cys Cys Leu Leu Pro Ser
20 25 30

Cys Leu Pro Ala Gly Gln Ser Val Asp Phe Pro Trp Ala Ala Val
35 40 45

Asp Asn Met Met Val Arg Lys Gly Asp Thr Ala Val Leu Arg Cys

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                50                  55                  60

Tyr Leu Glu Asp Gly Ala Ser Lys Gly Ala Trp Leu Asn Arg Ser
                65                  70                  75

Ser Ile Ile Phe Ala Gly Gly Asp Lys Trp Ser Val Asp Pro Arg
                80                  85                  90

Val Ser Ile Ser Thr Leu Asn Lys Arg Asp Tyr Ser Leu Gln Ile
                95                 100                 105

Gln Asn Val Asp Val Thr Asp Asp Gly Pro Tyr Thr Cys Ser Val
               110                 115                 120

Gln Thr Gln His Thr Pro Arg Thr Met Gln Val His Leu Thr Val
               125                 130                 135

Gln Val Pro Pro Lys Ile Tyr Asp Ile Ser Asn Asp Met Thr Val
               140                 145                 150

Asn Glu Gly Thr Asn Val Thr Leu Thr Cys Leu Ala Thr Gly Lys
               155                 160                 165

Pro Glu Pro Ser Ile Ser Trp Arg His Ile Ser Pro Ser Ala Lys
               170                 175                 180

Pro Phe Glu Asn Gly Gln Tyr Leu Asp Ile Tyr Gly Ile Thr Arg
               185                 190                 195

Asp Gln Ala Gly Glu Tyr Glu Cys Ser Ala Glu Asn Asp Val Ser
               200                 205                 210

Phe Pro Asp Val Arg Lys Val Lys Val Val Val Asn Phe Ala Pro
               215                 220                 225

Thr Ile Gln Glu Ile Lys Ser Gly Thr Val Thr Pro Gly Arg Ser
               230                 235                 240

Gly Leu Ile Arg Cys Glu Gly Ala Gly Val Pro Pro Pro Ala Phe
               245                 250                 255

Glu Trp Tyr Lys Gly Glu Lys Lys Leu Phe Asn Gly Gln Gln Gly
               260                 265                 270

Ile Ile Ile Gln Asn Phe Ser Thr Arg Ser Ile Leu Thr Val Thr
               275                 280                 285

Asn Val Thr Gln Glu His Phe Gly Asn Tyr Thr Cys Val Ala Ala
               290                 295                 300

Asn Lys Leu Gly Thr Thr Asn Ala Ser Leu Pro Leu Asn Pro Pro
               305                 310                 315

Ser Thr Ala Gln Tyr Gly Ile Thr Gly Ser Ala Asp Val Leu Phe
               320                 325                 330

Ser Cys Trp Tyr Leu Val Leu Thr Leu Ser Ser Phe Thr Ser Ile
               335                 340                 345
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Phe Tyr Leu Lys Asn Ala Ile Leu Gln
350

<210> 131
<211> 823
<212> DNA
<213> Homo Sapien

<400> 131
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cacatgggca caatttcaca ttcaagctcc ttatcctagg ctaattttat 100

attatgttaa atcacttgtt tttgttctca cggcttcctg cctgctatag 150

gcataattac gaggaagcag aacttctcca gaagcaagcg cacatgcgtt 200

ccaaaataag agcaaattcg ctctaaacac aggaaaagac ctgaagcttt 250

aattaagggg ttacatccaa ccccagagcg cttttgtggg cactgattgc 300

tccagcttct gcgtcactgc gcgagggaag agggaagagg atccaggcgt 350

tagacatgta tagacacaaa aacagctgga gattgggctt aaaataccca 400

ccaagctcca aagaagagac ccaagtcccc aaaacattga tttcagggct 450

gccaggaagg aagagcagca gcagggtggg agagaagctc cagtcagccc 500

acaagatgcc attgtccccc ggcctcctgc tgctgctgct ctccggggcc 550

acggccaccg ctgccctgcc cctggagggt ggccccaccg gccgagacag 600

cgagcatatg caggaagcgg caggaataag gaaaagcagc ctcctgactt 650

tcctcgcttg gtggtttgag tggacctccc aggccagtgc cgggcccctc 700

ataggagagg aagctcggga ggtggccagg cggcaggaag gcgcaccccc 750

ccagcaatcc gcgcgccggg acagaatgcc ctgcaggaac ttcttctgga 800

agaccttctc ctcctgcaaa tag 823

<210> 132
<211> 155
<212> PRT
<213> Homo Sapien

<400> 132
Met Tyr Arg His Lys Asn Ser Trp Arg Leu Gly Leu Lys Tyr Pro
1 5 10 15

Pro Ser Ser Lys Glu Glu Thr Gln Val Pro Lys Thr Leu Ile Ser
20 25 30

Gly Leu Pro Gly Arg Lys Ser Ser Ser Arg Val Gly Glu Lys Leu
35 40 45

Gln Ser Ala His Lys Met Pro Leu Ser Pro Gly Leu Leu Leu Leu
50 55 60

Leu Leu Ser Gly Ala Thr Ala Thr Ala Ala Leu Pro Leu Glu Gly
65 70 75

Gly Pro Thr Gly Arg Asp Ser Glu His Met Gln Glu Ala Ala Gly
80 85 90

Ile Arg Lys Ser Ser Leu Leu Thr Phe Leu Ala Trp Trp Phe Glu
95 100 105

Trp Thr Ser Gln Ala Ser Ala Gly Pro Leu Ile Gly Glu Glu Ala
110 115 120

Arg Glu Val Ala Arg Arg Gln Glu Gly Ala Pro Pro Gln Gln Ser
125 130 135

Ala Arg Arg Asp Arg Met Pro Cys Arg Asn Phe Phe Trp Lys Thr
140 145 150

Phe Ser Ser Cys Lys
155

<210> 133
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 133
tcagggctgc caggaaggaa gagc 24

<210> 134
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 134
gcaggaggag aaggtcttcc agaagaag 28

<210> 135
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 135
agaagttcca gtcagcccac aagatgccat tgtcccccgg cctcc 45

<210> 136

<211> 1875
<212> DNA
<213> Homo Sapien

<400> 136
gtcgtgtgct tggaggaagc cgcggaaccc ccagcgtccg tccatggcgt 50

ggagccttgg gagctggctg ggtggctgcc tgctggtgtc agcattggga 100

atggtaccac ctcccgaaaa tgtcagaatg aattctgtta atttcaagaa 150

cattctacag tgggagtcac ctgcttttgc caaagggaac ctgactttca 200

cagctcagta cctaagttat aggatattcc aagataaatg catgaatact 250

accttgacgg aatgtgattt ctcaagtctt tccaagtatg gtgaccacac 300

cttgagagtc agggctgaat ttgcagatga gcattcagac tgggtaaaca 350

tcaccttctg tcctgtggat gacaccatta ttggaccccc tggaatgcaa 400

gtagaagtac ttgctgattc tttacatatg cgtttcttag cccctaaaat 450

tgagaatgaa tacgaaactt ggactatgaa gaatgtgtat aactcatgga 500

cttataatgt gcaatactgg aaaaacggta ctgatgaaaa gtttcaaatt 550

actccccagt atgactttga ggtcctcaga aacctggagc catggacaac 600

ttattgtgtt caagttcgag ggtttcttcc tgatcggaac aaagctgggg 650

aatggagtga gcctgtctgt gagcaaacaa cccatgacga aacggtcccc 700

tcctggatgg tggccgtcat cctcatggcc tcggtcttca tggtctgcct 750

ggcactcctc ggctgcttct ccttgctgtg gtgcgtttac aagaagacaa 800

agtacgcctt ctcccctagg aattctcttc cacagcacct gaaagagttt 850

ttgggccatc ctcatcataa cacacttctg tttttctcct ttccattgtc 900

ggatgagaat gatgtttttg acaagctaag tgtcattgca gaagactctg 950

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cctggactta gccaccagag agctacattt taaaggctgt cttggcaaaa 1200

atactccatt tgggaactca ctgccttata aaggctttca tgatgttttc 1250

agaagttggc cactgagagt gtaattttca gccttttata tcactaaaat 1300

aagatcatgt tttaattgtg agaaacaggg ccgagcacag tggctcacgc 1350

ctgtaatacc agcaccttag aggtcgaggc aggcggatca cttgaggtca 1400

ggagttcaag accagcctgg ccaatatggt gaaacccagt ctctactaaa 1450

aatacaaaaa ttagctaggc atgatggcgc atgcctataa tcccagctac 1500

tcgagtgcct gaggcaggag aattgcatga acccgggagg aggaggagga 1550

ggttgcagtg agccgagata gcggcactgc actccagcct gggtgacaaa 1600

gtgagactcc atctcaaaaa aaaaaaaaaa aaattgtgag aaacagaaat 1650

acttaaaatg aggaataaga atggagatgt tacatctggt agatgtaaca 1700

ttctaccaga ttatggatgg actgatctga aaatcgacct caactcaagg 1750

gtggtcagct caatgctaca cagagcacgg acttttggat tctttgcagt 1800

actttgaatt tatttttcta cctatatatg ttttatatgc tgctggtgct 1850

ccattaaagt tttactctgt gttgc 1875

<210> 137
<211> 325
<212> PRT
<213> Homo Sapien

<400> 137
Met Ala Trp Ser Leu Gly Ser Trp Leu Gly Gly Cys Leu Leu Val
1 5 10 15

Ser Ala Leu Gly Met Val Pro Pro Pro Glu Asn Val Arg Met Asn
20 25 30

Ser Val Asn Phe Lys Asn Ile Leu Gln Trp Glu Ser Pro Ala Phe
35 40 45

Ala Lys Gly Asn Leu Thr Phe Thr Ala Gln Tyr Leu Ser Tyr Arg
50 55 60

Ile Phe Gln Asp Lys Cys Met Asn Thr Thr Leu Thr Glu Cys Asp
65 70 75

Phe Ser Ser Leu Ser Lys Tyr Gly Asp His Thr Leu Arg Val Arg
80 85 90

Ala Glu Phe Ala Asp Glu His Ser Asp Trp Val Asn Ile Thr Phe
95 100 105

Cys Pro Val Asp Asp Thr Ile Ile Gly Pro Pro Gly Met Gln Val
110 115 120

Glu Val Leu Ala Asp Ser Leu His Met Arg Phe Leu Ala Pro Lys
125 130 135

Ile Glu Asn Glu Tyr Glu Thr Trp Thr Met Lys Asn Val Tyr Asn
140 145 150

Ser Trp Thr Tyr Asn Val Gln Tyr Trp Lys Asn Gly Thr Asp Glu
155 160 165

Lys Phe Gln Ile Thr Pro Gln Tyr Asp Phe Glu Val Leu Arg Asn
170 175 180

Leu Glu Pro Trp Thr Thr Tyr Cys Val Gln Val Arg Gly Phe Leu
185 190 195

Pro Asp Arg Asn Lys Ala Gly Glu Trp Ser Glu Pro Val Cys Glu
200 205 210

Gln Thr Thr His Asp Glu Thr Val Pro Ser Trp Met Val Ala Val
215 220 225

Ile Leu Met Ala Ser Val Phe Met Val Cys Leu Ala Leu Leu Gly
230 235 240

Cys Phe Ser Leu Leu Trp Cys Val Tyr Lys Lys Thr Lys Tyr Ala
245 250 255

Phe Ser Pro Arg Asn Ser Leu Pro Gln His Leu Lys Glu Phe Leu
260 265 270

Gly His Pro His His Asn Thr Leu Leu Phe Phe Ser Phe Pro Leu
275 280 285

Ser Asp Glu Asn Asp Val Phe Asp Lys Leu Ser Val Ile Ala Glu
290 295 300

Asp Ser Glu Ser Gly Lys Gln Asn Pro Gly Asp Ser Cys Ser Leu
305 310 315

Gly Thr Pro Pro Gly Gln Gly Pro Gln Ser
320 325

<210> 138
<211> 2570
<212> DNA
<213> Homo Sapien

<400> 138
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ccgccatggc ccgcgcagcc ccgctgctcg ccgcgttgac cgcgctcctc 100

gccgccgccg ctgctggcgg agatgccccg ccgggcaaaa tcgcggtggt 150

tggggctggg attgggggct ctgctgtggc ccattttctc cagcagcact 200

ttggacctcg ggtgcagatc gacgtgtacg agaagggaac cgtgggtggc 250

cgcttggcca ccatctcagt caacaagcag cactatgaga gcggggctgc 300

ctccttccac tccctgagcc tgcacatgca ggacttcgtc aagctgctgg 350

ggctgaggca ccggcgcgag gtggtgggca ggagcgccat cttcggcggg 400

gagcacttca tgctggagga gactgactgg tacctgctga acctcttccg 450

cctctggtgg cactatggca tcagcttcct gaggctgcag atgtgggtgg 500

aggaggtcat ggagaagttc atgaggatct ataagtacca ggcccacggc 550

tatgccttct cgggtgtgga ggagctgctc tactcactgg gggagtccac 600

ctttgttaac atgacccagc actctgtggc tgagtccctg ctgcaggtgg 650

gcgtcacgca gcgctttatt gatgatgtcg tttctgctgt cctgcgggcc 700

agctatggcc agtcagcagc gatgcccgcc tttgcaggag ccatgtcact 750

agccggggcc caaggcagcc tgtggtctgt ggaaggaggc aataagctgg 800

tttgttccgg tttgctgaag ctcaccaagg ccaatgtgat ccatgccaca 850

gtgacctctg tgaccctgca cagcacagag gggaaagccc tgtaccaggt 900

ggcgtatgag aatgaggtag gcaacagctc tgacttctat gacatcgtgg 950

tcatcgccac ccccctgcac ctggacaaca gcagcagcaa cttaaccttt 1000

gcaggcttcc acccgcccat tgatgacgtg cagggctctt tccagcccac 1050

cgtcgtctcc ttggtccacg gctacctcaa ctcgtcctac ttcggtttcc 1100

cagaccctaa gcttttcccc tttgccaaca tccttaccac agatttcccc 1150

agcttcttct gcactctgga caacatctgc cctgtcaaca tctctgccag 1200

cttccggcga aagcagcccc aggaggcagc tgtttggcga gtccagtccc 1250

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tcagtgcaga cagctgagtg gcaggcccat cccctctatg gctcccgccc 1350

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Val	Val	Gly	Ala	Gly	Ile	Gly	Gly	Ser	Ala	Val	Ala	His	Phe	Leu	
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Met	Gln	Asp	Phe	Val	Lys	Leu	Leu	Gly	Leu	Arg	His	Arg	Arg	Glu	
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Val	Val	Gly	Arg	Ser	Ala	Ile	Phe	Gly	Gly	Glu	His	Phe	Met	Leu	

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Tyr Ala Phe Ser Gly Val Glu Glu Leu Leu Tyr Ser Leu Gly Glu
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Ser Thr Phe Val Asn Met Thr Gln His Ser Val Ala Glu Ser Leu
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Leu Gln Val Gly Val Thr Gln Arg Phe Ile Asp Asp Val Val Ser
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Phe Ala Gly Ala Met Ser Leu Ala Gly Ala Gln Gly Ser Leu Trp
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Ser Val Glu Gly Gly Asn Lys Leu Val Cys Ser Gly Leu Leu Lys
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Leu His Ser Thr Glu Gly Lys Ala Leu Tyr Gln Val Ala Tyr Glu
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Ala Thr Pro Leu His Leu Asp Asn Ser Ser Ser Asn Leu Thr Phe
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Ala Gly Phe His Pro Pro Ile Asp Asp Val Gln Gly Ser Phe Gln
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Pro Thr Val Val Ser Leu Val His Gly Tyr Leu Asn Ser Ser Tyr
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Phe Gly Phe Pro Asp Pro Lys Leu Phe Pro Phe Ala Asn Ile Leu
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Thr Thr Asp Phe Pro Ser Phe Phe Cys Thr Leu Asp Asn Ile Cys
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Pro Val Asn Ile Ser Ala Ser Phe Arg Arg Lys Gln Pro Gln Glu
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Ala Ala Val Trp Arg Val Gln Ser Pro Lys Pro Leu Phe Arg Thr
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Arg Phe Ala Leu His Asp Gln Leu Phe Tyr Leu Asn Ala Leu Glu
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Trp Ala Ala Ser Ser Val Glu Val Met Ala Val Ala Ala Lys Asn
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